

# STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number:130245

TO: Jeffrey Parkin

Location: REM-3D39/3E18

Art Unit: 1648

Thursday, September 02, 2004

Case Serial Number: 10/001407

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

### Search Notes

Dear Examiner Parkin,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



LING PRICE BLANK (1370)



130245

From:

Parkin, Jeffrey

Sent:

Wednesday, August 18, 2004 10:16 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence Search: U.S. Serial No. 10/001,407

Please search SEQ ID NOS.: 10 and 15 from U.S. Serial No. 10/001,407 (Yang, Y., and T. Burrell) v. all relevant databases, including interference. SEQ ID NO.: 10 corresponds to a region of the HIV-2 genome so it will probably pick up a large number of full-length sequences. Can you limit the search results to pick up ONLY nucleic acid sequences that are =<100 nucleotides in length for both sequences?

Place results on both disk and paper.

Thanks!

JSP REM 3D39 AU 1648 2-0908

STAFF USE ONLY
Searcher:
Searcher Phone: 2-
Date Searcher Picked up:
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Searcher Prep/Rev. Time:
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Type of Search	
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Yang, Y.Y. and Burrell, T.A. Compositions and methods f 2 (hiv-2)

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#### RESULT 1 AX498422 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM Result No. REFERENCE 00000000 O 15 14.8 14.8 14.8 14.4 14.4 14.4 16.6 16.6 16.6 16.6 16.2 15.4 15.4 15.4 15.4 15.4 15.4 AX498422 Sequence AX498422 Human immunodeficiency virus 2 (HIV-2) Human immunodeficiency virus 2 Viruses; Retroid viruses; Retroviridae; AX498422.1 GI:23343300 lentivirus group. % Query Match $\begin{array}{c} 1111\\ 1000\\$ 100 10 Length from Patent 멂 **თთთთთთთთთ** E30948 AX498425 BD151898 AR011291 AI17929 AI498430 AXXII2460 AXXII2461 HIVLTRAAB AR015482 AX015482 AX015482 AX015482 AX015482 AX0158034 HIVLTRAABI AR040804 AF040804 AXXI19961 AX498422 AX498421 AX498421 AX498427 HIVLTRAAJ AX498426 AX498431 AX498431 AR093423 AY102626 AX347672 E33310 S63302 ij 25 bp WO0234951. SUMMARIES ALIGNMENTS DNA Lentivirus; linear AX498426 Sequence AX498431 Sequence AX693423 Sequence E30948 Amplificati AX498425 Sequence E310489 Monhuman AR011291 Sequence E117929 Sequence EX112460 Sequence AX112461 Sequence AX112461 Sequence AX112461 Sequence M74754 Human immun M74755 Human immun M74756 Human immun M74757 Human immun M74759 Sequence E0210949 Anti-viral AX119975 Sequence AX0136024 Sequence AX138024 Hepatitis AF0400854 Hepatitis AF0400854 Hepatitis AF0400854 Hepatitis AF0400854 Hepatitis AF0400854 Hepatitis AF0400854 Hepatitis AX498422 Sequence AX498420 Sequence AX498421 Sequence AX498427 Sequence AX498427 Sequence M74764 Human immun AXII19964 Sequence AXI38017 Sequence AYI102626 Homo sapi AX347672 Sequence E33310 DsbA/DsbB/D Description S63302 vpu=membran Primate PAT 26-SEP-2002

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Human immunodeficiency virus 2
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Human immunodeficiency virus 2 (HIV-2)
Human immunodeficiency virus 2
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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The sequence of human immunodeficiency virus type 2 circle junction suggests that integration protein cleaves the ends of linear DNA asymmetrically
J. Virol. 65 (7), 3906-3910 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB
Pred. No. 0.8;
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WO0234951.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Score 25; DB 6; Length 34; Pred. No. 0.84; Indels
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Indels <u>,</u> Gaps

0

for detecting human immunodeficiency virus DNA linear PAT 26-SEP-2002

/organism="synthetic construct"
/mol\_type="unassigned DNA"
/db\_xref="taxon:32630"
/note="Tyromoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary priseguence" primer

6; 0 Length Indels 52 0 Gaps

0

88 bp DNA linear VRL 02-AUG-1 partial sequence, clone 1. VRL 02-AUG-1993

source text: Human immunodeficiency Location/Qualifiers virus type

/proviral
/mol\_type="genomic DNA"
/db\_xref="taxon:11709" organism="Human immunodeficiency

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SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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AX498426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                         Sequence 19 from Patent AX498431
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                                                                                                                                                                                                                                                                                                                                                           1 CGGGCGCCAACCTGCTAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions and methods for detecting 2 (hiv-2)
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Human immunodeficiency virus 2
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Sequence 14 from Patent
AX498426
                                                                                                                       Patent: WO 0234951-A 19 02-MAY-2002;
Gen-Probe Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 0234951-A 14 02-MAY-2002;
Gen-Probe Incorporated (US)
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                                                                                                                                                                                                               synthetic
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                                                                                                                                                                                                    artificial sequences.
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                                                       /note="T7 promoter primer having a
appended at the 5' end of an HIV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Human immunodeficiency virus
/mol_type="unassigned DNA"
/db_xref="taxon:11709"
                                             sequence"
                                                                            organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                               construct
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100.0%; Pr
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100.0%; Pred. No. 2.1e+03
tive 0; Mismatches 0
  72.0%;
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Pred. No.
  Score
Pred.
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J. DB 14;
Mo. 6e+02;
Mismatches
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WO0234951.
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WO0234951.
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No.
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1.9e+03;
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Matches
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CC Topology: Linear;
FH Key
FT source
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AR093423
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John, W.B., Suzan, M.A., Ann, E.K., Eric, B.R. and Thomas, J.K.
John, W.B., Suzan, M.A., Ann, E.K., Eric, B.R. and Thomas, J.K.
Amplification and detection of HIV-1 and/or HIV-2
Patent: JP 199069987-A 31 16-MAR-1999;
ORTHO CLINICAL DIAGNOSTICS INC
OS Unidentified
ON JP 199069987-A/31
PD 16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      Amplification and detection of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amplification and detection of HIV-1 and/or HIV 2 Patent: US 6001558-A 31 14-DEC-1999; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                   unidentified
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Backus, J.W., Atwood, S.M., Casey, A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR093423
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milarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                    assified
                                                                                                                                                                   24-JUN-1998 JP 1998177059
55-JUN-1997 US
60/050759
JOHN WESLEY BACCHUS, SUZAN MERISSA ATTWOOD, ANN ELIZABETH ERIC BRICE RASMUSSEN, THOMAS JOSEPH KAMINZU
C12N15/09,C12Q1/68,G01N33/566,G01N33/569,C12N15/00 CC
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                                    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                       /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                           GI:13025679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="unknown"
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68.0%;
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Pred. No.
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Score 17;
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Length 22;
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Bynthetic construct
stylicial sequences.

1 (bases 1 to 32)
1 (bases 1 to 32)
2 Shinohara, K., Sakai, K. and Honda, M.
Nonhuman primatal model of acquired immunodeficiency syndrome
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE
ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH
ON Artificial Sequence
ON Artificial Sequence
ON ARTIGORAL SAFETY AND RESEARCH
PD 04-UTW-2002
PP 27-NOV-2002
PP 27-NOV-2002
PF 27-NOV-2003 JP 200360274
PI KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA
PC C12N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/50/
PC (C12N7/00, C12R1:93), (C12N7/02, C12R1:93), C12N15/00 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0%; I hes 17; Conservative 0;
                                                                                                  PC (C12N7/00,C12R1:93),(C12N7/02,C12R1:93),C12N15/00 CC Description of Artificial Sequence: artificially synthesis
                                                                                                                                                                                                                                                                                                                                                                        BD161898.1 GI:27867656 JP 2002159296-A/7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang, Y.Y. and Burrell, T.A.
Compositions and methods for detecting
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synthetic construct
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Sequence 13 from Patent
AX498425
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                                                                                                                                         27-NOV-2000 JP 2000360274
KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA
C12N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/50//
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ilarity 82.6%;
Conservative
                           /organism='Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO 0234951-A 13 02-MAY-2002;
be Incorporated (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:12630"
/note="Primer mismatches HIV-2 sequence by deletion
nucleotide"
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Pred. No. 1e+04;
0; Mismatches 4; Indels
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                                                                                                                                          1 (bases 1 to 42)

Paoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K., Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E., Cox,W.I., Audonnet,J.-C.F. and Gettig,R.R.

NYVAC vaccinia virus recombinants comprising heterologous inserts Patent: US 5494807-A 160 27-FEB-1996;
                                                                                                                                                                                                                                                                                                                          Sequence
I17929
                                                                                                                                                                                                                                                Unclassified.
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1 (bases 1 to 42)

Raoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K., Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E., Cox,W.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.

Modified recombinant vaccinia virus and expression vectors thereof Patent: US 5762938-A 160 09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Sequence 160 from patent US
AR011291 GI:3969281
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/mol_type="unassigned DNA"
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/organism="synthetic coi/mol_type="genomic DNA"
/db_xref="taxon:32630"
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82.6%;
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patent US 5494807.
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Query Match Best Local S Matches 19

Similarity

REFERENCE AUTHORS TITLE

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Gen-Probe

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                                                         Query Match 64.8
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                                                                                                                                                                                                                             Braun, A., Koester, H., van den Boom, D., Ping, Y., Rodi, C., He, L., Chiu, N. and Jurinke, C.
Methods for generating databases and databases for identifying polymorphic genetic markers
Patent: WO 012787-A 108 19-APR-2001;
                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         AX112460 100 bp
Sequence 108 from Patent W00127857.
AX112460
AX112460.1 GI:13939219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 0234951-A 18 02-MAY-2002;
Gen-Probe Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang,Y.Y. and Burrell,T.A.

Compositions and methods for detecting human immunodeficiency virus
2 (hiv-2)
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Sequence 18 from Patent WO0234951.
AX498430
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                GGGCGCCAACCTGCTAGGGAT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="T7 promoter primer having a promoter sequence appended at the 5' end of the sequence given as SEQ ID NO:13"
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                                                                                                                                                                                                   Location/Qualifiers
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85.7%; Pred. No. 1.3e+04;
tive 0; Mismatches 3; Indels
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Search completed: August 31, 2004, 02:04:24 Job time : 527.623 secs THIS PACE BLANK (USPTO)

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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

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ABK93886 standard; DNA;

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30-MAR-2001; 2001US-0280058P.
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(first entry)
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The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs wit 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C

With

Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target

duplex.

Claim 10; Page 25; 58pp; English.

WPI; 2002-489953/52.

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The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a combatter probe and detectable label, hybridising HIV-2 NA with the probe to form probe and detectable label, hybridising HIV-2 NA with the considerable to form probe the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA considerable serum and also as components of multiplex amplification creactions that synthesise amplicons corresponding to polymucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HBN) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the vive field)
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                                                                                                                                                                                                                                                                                                        Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
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30-MAR-2001; 2001US-0280058P.
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                                                                                                The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonuclectides, amplifying HIV-2 nuclectide Sequence, and detecting the amplified NA; or providing a CC probe to form probe and detectable label, hybridising HIV-2 NA with the CC probe to form probe:target duplex, and detecting the duplex. The method CC product such as plasma or serum, and also for detecting subtypes A, B, C CC in blood serum and also acomponents of multiplex amplification CC reactions that synthesise amplicons corresponding to polynuclectides of CC curselated viruses, e.g. HIV-1, hepatitis B virus (HAV) and hepatitis C CC invention. (Updated on 29-AUG-2003 to standardise os field)
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                                                                                                                                                                                                                                                                                                                                        Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 2 detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENP-) GEN-PROBE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200234951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2003
26-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK93884;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ϋ́
                                                   Similarity
CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                                                                                                                                                                                                                Burrell TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGCGCCAACCTGCTAGGGATTTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGCGCCAACCTGCTAGGGATTTT 25
                                  100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative 0
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(first en
                                                                               A; 10 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                  0,
                              Score 25; DB
Pred. No. 0.0
0; Mismatches
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Pred. No. 0.011;
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                                              0.011;
                                                          DB
                                                          6
                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6,
                                                       Length 34;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
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                             <u>,,</u>
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                             Gaps
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RESULT 5
ABK93890
ID ABK9
XX
AC ABK9
DT 29-A
DT 26-A
XX
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                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                          The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonuclectides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HEV) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang
             29-AUG-2003
26-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
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26-AUG-2002
                                                           ABK93890;
                                                                                                                                                                                                                                                                               Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 25; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-489953/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2001; 2001WO-US045396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 2 detection probe #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK93891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK93891 standard; DNA; 52
                                                                                     ABK93890 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ϋ́
                                                                                                                                                               28
                                                                                                                                                                                           ب
                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEN-PROBE INC.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                             CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                              CGGGCGCCAACCTGCTAGGGATTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burrell TA;
                                                                                                                                                                                                                         Conservative
             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                     DNA;
                                                                                                                                                                                                                                       100.0%;
                                                                                      25
                                                                                      ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                     Score 25; DB 6;
Pred. No. 0.012;
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis B virus; HBV
                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                     Length 52;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         0
                                                                                                                                                                                                                      Gaps
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ABK93895
ID ABKX
XX
AC ABKS
ABK93895
ABKS
ABK93895
ABKS
ABK93895
ABKS
ABK93895
ABKS
ABK93895
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ABK93895
ABKS
AC ABCS
AC ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C virus (HCV). ABK93877-ABK33910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                       29-AUG-2003
26-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                    ABK93895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-489953/52.
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30-MAR-2001; 2001US-0280058P.
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                                                                                                                                                   hepatitis C virus;
                                                                                                                                                                                Human
                                                                                                                                                                                                                                             Human immunodeficiency virus type 2 detection probe #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK93895 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 25; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001; 2001WO-US045396
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                                                                                                                                                   immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV
itis C virus; HCV; probe; ss.
                                                                                         immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGCGCCAACCTGCTAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGCGCCAACCTGCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 3 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72. V.,
100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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WO200234951-A2

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RESULT 7
AAV63697
ID AAV6
XX AAV6
XX AAV6
XX II-M
XX II-M
XX PCR
XX CO-a
XX CO-a
XX Synt
CO Huma
XX Synt
XX EP88
PN EP88
PN EP88
XX EP88
XX EP88
XX GO-T
XX GO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                    Backus JW,
                                                    (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
                                                                                                                   25-JUN-1997;
                                                                                                                                                                24-JUN-1998;
                                                                                                                                                                                                                 30-DEC-1998.
                                                                                                                                                                                                                                                                 EP887427-A2
                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                    HIV-1; HIV-2; det co-amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV63697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV63697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 25; 58pp; English.
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30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGGGCGCCAACCTGCTAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ceeeccaacciectae 58
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             Atwood SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burrell TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1larity 100.0%; FCONSERVATIVE 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                  detection; Acquired Immunodeficiency Syndrome; AIDS;
                                                                                                           97US-0050759P.
                                                                                                                                                          98EP-00304959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0242620P.
2001US-0280058P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplify HIV-2 sequences.
       Casey AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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Pred. No.
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     Rasmussen
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     EB,
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Cummins
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RESULT 8
ALK93889
ALK93889
XX ABK9
XX ABK9
XX 29-Ai
DT 26-Ai
XX Huma
XX Huma
XX Hepa
XX Huma
XX Hopa
XX WO20
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XX USA
PF 22-O
XX USA
XX WPI;
XX GEN
XX YANG
PR 30-M
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PR 30-M
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PR 3
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Best Local
The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs will st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a
                                                                                                                                                              Claim 10; Page
                                                                                                                                                                                                              Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
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26-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2 detection probe #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present PCR primer is used to amplify human deficiency type 2 (HIV-2) nucleic acids. The specification also describes primers and probes for HIV-1 and HIV-2. The primers and probes are useful for amplifying and biological samples, and HIV-2 and all their subtype nucleic acids in Acquired Immunodeficiency Syndrome (AIDS). The primers are able to detect all HIV-1 and HIV-2 subtypes without detecting non-related viruses. The primer sets for HIV-1 and HIV-2 are compatible with each other, and can more than one primer set to amplification assay for HIV-1 and HIV-2. Using overlap a common probe region maximises strain sensitivity and robustness overlap a common probe region maximises strain sensitivity and robustness
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17; Conserv
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                                                                                                                                                                 25;
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(first entry)
                                                                                                                                                      58pp; English.
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Pred. No. 1.1e+02;
0; Mismatches 0;
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ARESULT 9
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ID AAQ353
XX AAQ35
XX AAQ35
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                                                                                                                                                                                                                                        The env gene of HIV was subjected to in vitro mutagenesis to remove the sequences encoding the rex protein and the LTR region from the 3' end of the gene and to delete the putative immuno-suppressive (18) region (amino acids 583-599). Mutagenesis was performed using primers LTR2 and MUENSVISR using pIBI25mutenv8 as template. Mutagenised clones were identified by hybridsation and restriction analysis. See also AAQ35328-437. (Updated on 25-MAR-2003 to correct PN field.)
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11-JUN-1992;
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18-MAY-1993
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                                                                                                                                                                                      Sequence 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified recombinant virus with inactivated non-essential genetic functions - comprises e.g. vaccine or avipox virus, used as HIV vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUENSVISR, a mutagenesis primer for env gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCGCCACCTGCTAGGGATTTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 49; 159pp; English.
                                                                                                                                                                                         BP;
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                                                                                   Conservative
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92US-00897382.
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82.6%;
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                                                                                                         66.4%;
82.6%;
                                                                                                                                                                                      8 C; 15 G; 11 T; 0 U; 0 Other;
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Pred. No. 1.8e+02;
                                                                                                            Score 16.6;
Pred. No. 2e
                                                                                     Mismatches
                                                                                                            2e+02;
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                                                                                                                                     DB 2;
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                                                                                                                                     Length 42;
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AAH02411;

AAH02411 standard;

DNA;

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RESULT 10
ABK93894
ID ABK93
XX ABK93
XX ABK93
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                                                                                                                                                                                                                                                                                                          The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with CC ist and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a CC hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the probe of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA Ci in blood serum and also as components of multiplex amplification CC reactions that synthesise amplicons corresponding to polynucleotides of currelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C corrus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the curve that the control of the curve that synthesise amplication of the currelated viruses.
                                                                                                                                Matches
                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:tar
                                                                                                                                                                                                                                                       Sequence 57 BP; 17 A; 14 C; 14 G; 12 T; 0 U; 0 Other;
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26-AUG-2002
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30-MAR-2001; 2001US-0280058P.
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                                     GGCGCCAACCTGCTAGGGATTTT 25
GGGCGCCACCTGCTAGGGATTTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCATCAAGCAGCTAGGGATTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burrell TA
                                                                                                                             Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58pp; English.
                                                                                                                                                     82.6%;
                                                                                                                             0,
                                                                                                                                                           Score 16.6;
Pred. No. 2
                                                                                                                          Mismatches
                                                                                                                                                           2.1e+02;
                                                                                                                                                                                          DB 6;
                                                                                                                                                                                          Length
                                                                                                                                Indels
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RESULT 12
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Best Local S
Matches 18
             13-OCT-2000; 2000WO-US028413
                                                                                        gurg
                                                                                                                    Human
                                  19-APR-2001.
                                                     WO200127857-A2
                                                                      Homo sapiens.
                                                                                               Database; polymorphism;
                                                                                                                                      12-JUN-2001
                                                                                                                                                                       AAH02412 standard; DNA;
                                                                                                                                                        AAH02412;
                                                                                                                                                                                                                                                                                                      The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 303; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Producing a database for identifying polymorphic genetic n comprises obtaining data relating to members of a healthy entering the information into a database.
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Chiu l
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10-JUL-2000;
19-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database; polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l3-OCT-1999;
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                                                                                        response,
                                                                                                           Factor XIII coding sequence fragment SEQ ID NO: 109.
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                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                               GGGCGCCAACCTGCTAGGGAT 22
                                                                                                                                                                                                                  GGGCGTCAACCTGCAAGGTAT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENOM INC
                                                                                                                                                                                                                                                                                              100 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jurinke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koester H,
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 99US-0159176P.
; 2000US-0217251P.
; 2000US-0217658P.
; 2000US-00663968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequence fragment SEQ ID NO: 108.
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                                                                                                                                                                                                                                                               64.8%;
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                                                                                               SNP;
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                                                                                         human; genetic marker; disease;
                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                     Pred. No. 3.7e
0; Mismatches
                                                                                                                                                                                                                                                               Score 16.2; DB 4;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                         28 G; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; genetic marker; disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boom
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                                                                                         infection,
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RESULT 13
ACC00078 s
XX ACC00078;
ACC00078 s
Primer #4
XX Human; ret
XX Human; ret
XX Homo sapic
XX Homo sapic
PN CN1380303.
XX CN1380303.
XX ACC S1-APR-20;
XX HAN-) S;
XX ACC S1-APR-203
XX AC
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Best Local S
Matches 18
                                                                                                Example 4; Page 21; 35pp;
                                                                                                                                                                                         WPI; 2003-222536/22
                                                                                                                                                                                                                                                                                                                                                        11-APR-2001; 2000CN-00125808
                                                                                                                                                                                                                                                                                                                 11-APR-2001, 2000CN-00125808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN1380303-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; retinoblastoma binding protein 34.54; tumour; ss; primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a database of human samples obtained free healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the sample by parameters such as age, sex and ethnicity. This is useful in linkin markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 100 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population and entering the information into a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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Chiu r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1999; 99US-0159176P.
10-JUL-2000; 2000US-0217251P.
10-JUL-2000; 2000US-0217658P.
19-SEP-2000; 2000US-00663968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SEQU-) SEQUENOM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                         polypeptide-human retinoblastoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                          SHANGHAI BIOWINDOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCGTCAACCTGCAAGGTAT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Page 303; 304pp; English.
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Jurinke C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related
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85.7%;
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Pred. No. 3.7e+02;
0; Mismatches 3
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linking
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The present invention relates to human retinoblastoma binding protein 34.54, used to treat various tumours. The present sequence represents primer related to human retinoblastoma binding protein encoding sequen

SS

Sequence

**3**3

BP;

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7 C;

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7

T; 0 U; 0 Other;

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RESULT 14
ABAO5816/c
ID ABAO58
XX ABAO58
XX ABAO58
XX Human 1
XX Human 1
XX Gene L
XX Gene L
XX Gene L
XX Gene L
XX Human 1
XX Human
RESULT 15
AAT68636/c
ID AAT686
XX
AC AAT686
XX
AC AAT686
XX
VI/T2
XX
VI/T2
XX
UNA in
KW DNA in
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Best Local S
Matches 18
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human ubiquitin-like protein 14. The sequences can be used in the treatment of cancer, haemopathy and HIV infection. The present sequence is a probe for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ubiquitin-like protein 14; cancer; haemopathy; HIV infection; gene therapy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41 BP; 6 A; 11 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 19 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide-human ubiquitin-similar protein 14 for treating cancer, hematopathy, and human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-056326/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2000; 2000CN-00115234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000CN-00115234.
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  DNA integration; LexA; gene therapy; oncogene inactivation; retrovirus; HIV-1; FIV; integrase; ss.
                                                                                    V1/T2 substrate for integration assay.
                                                                                                                                              14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BODE-)
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                                                                                                                                                                                                                                                          AAT68636 standard; DNA; 33 BP
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17; Conserv
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Search completed: August 31, Job time: 166.935 secs
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                                                                                                                                                                                                                                                                                                                                                                 Fusion protein comprising retroviral integrase and DNA binding regions useful for integrating donor DNA into specific sites on target DNA, especially for inactivating oncogene(s) or inserting therapeutic genes.
                                                                                                                                                                     Sequence 33
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-310594/28
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                                                                                  TITLE
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Trichoderma reesel EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
                                                                                                                                                                                                                                                                    14
                                                                                                                                                                           CF885516 62 bp mRNA linear EST 31-OCT-2003 tric082xk23.bl1 T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric082xk23, mRNA sequence. CF885516
                                                                                                               Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocrea.
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 62)
                                                                                                 Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M.
                                                                                                                                                                  CF885516.1 GI:38140198
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CG712371
BZ380126
R82154
D86884
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HSWC24E111
BZ595658
CG791268
AA513131
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CG717331
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BJ057939
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F33772
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AZ5216272
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AU106807 AU106807
CG717331 1119048A0
CG554070 OST167335
CG512760 OST167335
CG512760 OST83993
AA778887 af86f10.s
CG407857 OST23557
AG217446 Drosophil
BI908831 603066402
AG219169 Drosophil
BI014256 am50d10.s
BU816046 NO59E07 P
BZ763567 SALK 1193
AT006310 AT006310
AA491818 ng16b12.s
CK108605 1044P93 P
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BJ057936 G03063502
AA065383 m151e06. r
AZ600786 1M041BF15
CG399846 0150423-0
CL002253 0250069-0
U44135 ENU44135 As
F33772 H5PD27429 H
BM126072 if05b10.x
AZ921627 1006030G0
CB209994 OML00274
CB211074 OML01354
CB211075 OML04145
BH913033 3526 1 38
AA566995 1049 F051
CG712371 111902650
BZ380126 SALK, 1146
R82154 5E5 Chromos
D86884 Human exon
AJ547093 Drosophil
X8257093 Drosophil
X8257093 Drosophil
X8259568 SALK, 0894
CG781268 1123044C0
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                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 86.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GCGCCAACCTGCTAGGGATTTT 25
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             /clone_lib="NCI_CGAP_CO3"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site 2: Ecc RI; lst strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo (dT) primer. Double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Ecc RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:880802"
/sex="pooled"
                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"

[mol_type="mRNA"
                                                                                                                                                                                                             tissue_type="colon"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev_stage="mycelia"
| Cone_lib="T.reesei mycelial culture, Version 6 October
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clone="tric082xk23"
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Pred. No. 1.1e+04;
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: custom primer used High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Al256079 82 bp mRNA linear EST 12-NOV-1998 ui94912.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890118 3' similar to SW:COX3_RAT P05505 CYTOCHROME C OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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19; Conserva
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/clone_lib="Sugano mouse liver mlia"
/note="forgan: liver; Vector: pMRS18S-FL3; Site_1: DraIII
/note="forgan: liver; Vector: pMRS18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pMRS18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:1890118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                        dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                               sex="female"
                                                                                                                                                                                                                                                                                                                                                                lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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76.0%;
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Pred. No. 1.6e+04;
); Mismatches 6;
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Query Match Best Local Similarity

57.6%; 75.0%;

Score 14.4; DB 9; Pred. No. 4.2e+04;

Length 82;

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JOURNAL COMMENT
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AUTHORS
TITLE
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CB165114/c
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                    48
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CB165114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Rosellini, D.
Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barone, P., Rosellini, D. and Veronesi, F.
Isolation of expressed sequence tags from developing female sterile and female fertile alfalfa plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Medicago sativa
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44 Alfalfa developing flower bud library Medicago sativa cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borgo XX giugno 74, 06121, Perugia, Italy
Tel: +390755856211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Perugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
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                                                                                                                 Similarity
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                                                       GGCGCCAACCTGCTAGGGATTTT 25
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                                                                                                Conservative
                                                                                                                                                                                       /clone lib="Alfalfa developing flower bud library"
/clone lib="Cryan: Developing flower buds; Vector: Invitrogen
/note="Cryan: Developing flower buds; Vector: Invitrogen
PCR4 TOPO Vector; This EST was obtained with the CDNA-AFLP
method (Bachem et al.Plant Journal 9:745-753, 1996). Total
RNA was extracted from three female fertile and three
female sterile alfalfa plants from an F1 population
obtained by crossing the plants B17 and P13 (Rosellini et
al. Theoretical and Applied Genetics, 97:1 289-1295,
1998). Equal amounts of RNA from each fertile or sterile
plant were bulked and used for the CDNA-AFLP protocol.
The restriction endonucleases EcoRI and MseI were used.
Bands that were polymorphic between the female sterile and
female fertile bulks were isolated from the polyacrilamide
gel, cloned in a plasmid vector (Invitrogen PCR4 TOPO) and
sequenced using the M13F primer. The published sequence
begins and ends with the EcoRI (GAATTC) and MseI (TTAA)
recognition sequences, respectively. The technical help of
Francesco Panara is gratefully acknowledged."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roselli@unipg.it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/dev_stage="from ovule primordia to anthesis"
/lab_host="B.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="B17 x P13 F1 population"
/db_xref="taxon:3879"
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                                                                                                               Score 14.4; DB 14;
Pred. No. 4.4e+04;
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BJ057939
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AUTHORS
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RESULT

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AUTHORS
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Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Michael J. Brownstein, Emmert Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
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Kitayama,A.,
Kohara,Y.
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 72)
                                                                                                                                                                                                                                                   Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                        BJ057939
BJ057939.1 GI:17492296
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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wb81c10.xi NCI_CGAP_pr28 Homo sapiens cDNA clone IMAGE:2312082 3',
                                                                                                                                                                                                                                                                                                     Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAACCTGCTAGGGATTT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Glone lib="NCI CGAP Pr28"
//Glone lib="NCI CGAP Pr28"
//note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
//note="Organ: prostate; Vector: p18773D-Pac (Pharmacia)
//note="Organ: prostate; Vector: p18773D-Pac (Pharmacia)
//note="Organ: p18773D-Pac 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="male"
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                                Terasaka, C., Mochii, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.8%;
                                                                                                                                                                                                                                                                                                 (African clawed frog)
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Pred. No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                Ueno, N., Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 62;
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AUTHORS
TITLE
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VERSION
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BI907426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalla, Butheria, Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM11534 row: c column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
Center For Genetic Resource Information
Mational Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 41.
Location/Qualifiers
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Conservative
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                                                                                                                                                                                            /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212728"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone lib="NIH MGC 118"
/clone lib="NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
/note="Vector: pCMV-SPORT6; Site 2: EcoRV
/note="Vector: pCMV-SPORT6; Site 2: EcoRV
/note="V
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/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL103003"
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Pred. No. 5e+04;
0; Mismatches
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sapiens cDNA clone IMAGE:5212728 5',
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AUTHORS
                   Query Match
Best Local S
Matches 17
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SOURCE
ORGANISM
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AA065383/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 90.
Location/Qualifiers
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Mus. 1 (bases 1 to 96)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA065383 96 bp mRNA linear EST 0: ml51e06.rl Stratagene mouse testis (#937308) Mus musculus clone IMAGE:515554 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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EST.
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17; Conserv
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            56.0%;
ilarity 77.3%;
Conservative (
                                                                                                    /tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="50LR (kanamycin resistant)"
/clone_lib="Stratagene mouse testis (#937308)"
/note="0rgan: testis; Vector: pBluescript SK-; Sit EcoRI; Site_2: Xhol; Cloned unidirectionally. Pri Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR -5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adasequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
                                                                                                                                                                                                                                                                                                sex="males"
                                                                                                                                                                                                                                                                                                                 clone="IMAGE:515554"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.0%;
      Score 14; DB 9; Length 96;
Pred. No. 6.7e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 12;
Pred. No. 5.2e+04;
лВ э,
л.7е+04;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Louis,
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XR Vector;
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de 027. Note:
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3 GGCGCCAACCTGCTAGGGATTT

<u>,</u>

Gaps

RESULT 9 AZ600786/c

DEFINITION Focus

AZ600786

97

GSS 13-DEC-2000

밁

80

GGCGTCGACCTGCCCGGTATTT

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ACCESSION
VERSION
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                                                                                             Query Match
Best Local (
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                       Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 10000 Std Error: (
Plate: 0418 row: F column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ600786.1 GI:11722976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
GGCGCCAACCTGCTAGGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 97.
Location/Qualifiers
                                                                       Conservative
                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'lab_host="E. Coli strain XL10-Gold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
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                                                                                           56.0%;
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                                                                                             Score 14;
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d UUGC1M library Mus musculus genomic
                                                                                        DB 28;
6.8e+04;
                                                                       5
                                                                                                                 Length 97;
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CG399846/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                    CL002253 64 bp DNA linear GSS 19-
0280069-08C1-G08 UniformMu MuTAIL Library Zea mays genomic
0280069-08C1-G08, genomic survey sequence.
CL002253
CL002253 GI:40219332
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                       Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 64)
Latshaw,S., Tan,B-.C., Sett
Sequence tagged transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence flanking probable Mu insertion site in UniformMu line 0150423-03, Primer set: C Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Molecular and Ce
University of Florida
PO 110690 Gainesville,
Tel: 352-392-1928 x322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Donald R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
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Latshaw,S., Tan,B-.C., Sett
Sequence tagged transposon
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CG399846.1 GI:34398730
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             population
                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGCGCCAACCTGCTAGGGATTTT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4577"
/clone="0150423-03C1-0D1"
/clone="0150423-03C1-0D1"
/clone="UniformMu MuTAIL Library"
/clone lib="UniformMu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
/niserrions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
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  Settles,A.M. and McCarty,D.R. oson insertions from the UniformMu maize
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MUTAIL Library Zea mays genomic clone
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JOURNAL COMMENT

Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program

University of Florida PO 110690 Gainesville, FL 32611-0690, USA Tel: 352-392-1928 x322

FEATURES

Sequence flanking probable Mu insertion site in UniformMu line: 0250069-08, Primer set; C Class: transposon insertion site.

/organism="Zea mays"
/mol\_type="genomic DNA"
strain="W22 (ACR, bzl-m9)"
/cultivar="UniformMu"

Bource

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RESULT 14
BM126072/c
                               Shoor
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                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conservat
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MEDLINE
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F33772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                       source
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                       BM126072
                                                                                               3 GGCGCCAACCTGCTAGG 19
                                                                                   Ŋ
                                                                           GCCGCCAACCTCCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Valle G.
GRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW
http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 75)

Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. 1 (dentification of 4370 expressed sequence tags from a sequencing and filter hybridization skeletal muscle by DNA Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F33772
HSPD27429 HM3 Homo mapiens
F33772
F33772.1 GI:4819398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 CGGTCGGCCAGCTGCTAGGGCGTGT 39
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                           l Similarity
18; Conservat
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="s3000010H07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                    (tissue_type="pectoral muscle (after mastectomy)"
/clone_Tib="HM3"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                 55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Aspergillus nidulans cleistothecium"
/note="3'.-directed cDNA clones; single-pass sequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.2%; Score 13.8; DB 14; 72.0%; Pred. No. 7.6e+04;
                                                                            21
                                                                                                                        0
                                                                                                                 Score 13.8; DB 14;
Pred. No. 7.7e+04;
0; Mismatches 2;
                84
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s cDNA clone s3000010H07,
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             mRNA
      linear
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EST 12-MAR-2002
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mRNA sequence.
                                                                                                        Gaps
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                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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JOURNAL MEDLINE PUBMED COMMENT

REFERENCE AUTHORS TITLE

Lee,D., Lee,S., Hwang,H., Kim,J. and Chae,K. Quantitative analysis of gene expression in sexual structures of Aspergillus nidulans by sequencing of 3 directed cDNA clones FEMS Microbiol. Lett. 138 (1), 71-76 (1996)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

U44135.1 GI:1244798

RESULT 12 U44135 LOCUS DEFINITION

밁

63

CGGGCGCCAACCTGCTAGGGATTTT 25

Query Match
Best Local Similarity 72.0%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 7;

Length 64; Indels

0; Gaps

ç,

/db xref."taxon:4577"
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/clone="0260069-08C1-G08"
/clone="0260069-08C1-G08"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary spin columns and cloned into the TOPO PCR4 vector."

FEATURES

Contact: Keon-Sang Chae Chonbuk National University Chonju, 561-756, S. Korea Tel: +82-652-70-3340 Fax: +82-652-70-3345

source

chaeks@chonbuknms.chonbuk.ac.kr.
Location/Qualifiers

/organism="Emericella nidulans" |mol type="mRNA" |strain="FGSC4"

/db\_xref="taxon:162425" /clone="5E0101" /tissue\_type="cleistothecium" /cell\_type="Hull cell"

DEFINITION

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RESULT 15
AZ921627
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwhl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Bidocrine Pancreas Consortium Unpublished (2000)
                                                    AZ921627 94 b
1006030G08.x2 1006 - RescueMu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA :
Washington University Genome Sequencing Center For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
survey sequence.
AZ921627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ifO5b10.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA clone IMAGE:5675467 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                CGGGCACCAGCCTGCTA 48
                                                                                                                                                                                                                                            CGGGCGCCAACCTGCTA 17
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORTL; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT prining. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m, for clone orders contact: info@image.llnl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5675467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Islets of Langerhans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="Both"
                                                                                                                                                                                                                                                                                                                                             55.2%;
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                                                                                                                                                                                                                                                                                                                                             Score 13.8; DB 12;
Pred. No. 8e+04;
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                           94 bp
                                                    Grid G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Douglas Melton DNA sequencing by equencing Center For information
                                                  Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                   linear
                                                                                GSS 17-DEC-2001
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Search completed: August 31, 2004, 03:09:39 Job time: 1269.56 secs

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bource
                                                                                                             Local
                                                                                      18;
                                         1 CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: walbot@stanford.edu
Plate: 1006030 row: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ921627.1
GSS.
                                                                                                             Similarity
CAGGCGCCCGCCTCATTTGGATTTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to
                                                                                    Conservative
                                                                                                                                                                                                               /clone_lib="1006 - RescueMu Grid G"
/clone="Torgan: leaf; Vector: RescueMu (engineered from /note="Torgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu,' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with
                                                                                                                                                                                                 ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
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                                                                                                           55.2%;
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                                                                                                             Score 13.8; DB 28
Pred. No. 8.3e+04;
                                                                                  Mismatches
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المراسي الماليكيات عاقالما الالالتال

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 100
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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25
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                                                              cgggcgccaacctgctagggatttt 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-08-105-483-160

US-08-09-209-160

US-08-303-275-48

US-08-458-968E-20

US-08-458-968E-22

US-09-552-950-22

US-09-552-950-22

US-09-393-171-23

US-08-442-806-13

US-08-442-806-13

US-08-442-806-13

US-08-441-430-17

US-08-441-430-12

US-08-441-430-12

US-08-441-430-12

US-08-49-066-13

US-08-49-066-13
                         US-09-234-8278-10
US-08-019-870-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
               Sequence 31, Appl Sequence 160, App Sequence 160, Appl Sequence 62, Appl Sequence 22, Appl Sequence 21, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 31, Appl Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                       ; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-102-830-31
S
                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                TELEFAX: 908-524-2808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OGDEN, STASIA L
REGISTRATION UNMBER: 36,228
REFERENCE/DOCKET NUMBER: CDS-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-524-2819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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US/09/102,830

CDS-137/SLO

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CGGGCGCCAACCTGCTA 17

68.0%; Score 17; DB ilarity 100.0%; Pred. No. 12; Conservative 0; Mismatches

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Length 22; Indels

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RESULT 1  Sequence 31, Patent No. 6 GENERAL INF APPLICANT APPLICANT APPLICANT TITLE OF TITLE OF CORRESPON ADDRESS STREET: STATE: COUNTRY		<u>υ</u> .	44	4 2	Ξ	6	9	<b>6</b>	3 ŏ	ั้ง	4	ພັ	2	ĭ	õ	2 2 0 8
T 1 -102-830-31 Nuence 31, Applence 31, Applence 31, Applend in Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Nutrice OF INVITILE OF INVITITE OF INVITITE OF STREET: OF			12.6		12.6			12.8			12.8					13 13
1 101558 RMATION: BACKUS, ATWOOD, CASEY, RASMUSS CUMMING CUMMING ROUNTION NVENTION N		50.4	50.4	۰.	50.4	?		-:	51.2	۲.		:		1.		52.0
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N AND PLAZA	ALIGNMENTS	US-09-234-874A-	US-09-113-750A-48	US-08-387-805-14	US-09-336-946B-	US-09-103-875-5	US-08-866-340-49	US-09-434-122-56	US-08-485-246A-2	US-08-127-721A-	US-08-476-176B-	US-09-171-755B-14	US-08-639-763-14	US-09-422-978-739	980	US-08-484-322-3
DETECTION OF		-22	22 8	14	-64	55	49	5 6	7 7 6	-23	-23	-14	14	739	12	81
1-ЛІН		Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
		22,	2 4	14,	64,	55,	49,	5 6	7 6	23,	23,	14,	14,	739,		» (J
		Appl						Appl			Appl			), Āpp	App1	App1

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US-08-709-209-160
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                                                                                                                                                                       Sequence 160, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-105-483-160
                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                               APPLICANT: PAOLECTI, ENZO
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Paolet
                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE; Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
 COUNTRY:
                                              STREET:
                                                      ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer
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CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/105,483 FILING DATE: 12-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Curtis, Morris & Safford
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                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160, Application US/08105483
o. 5494807
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                                            530 Fifth Avenue
USA
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; Pred. No. 22;
0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILLING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.
FILING DATE: 11-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Paolet
APPLICANT: Tartag
APPLICANT: Cox, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                       STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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    Application US/08303275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840-3333
                                                                 US 07/897,382
                                                                                                                                     US/08/303,275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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REFERENCE/DOCKET NUMBER: 454310-2420

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US-08-458-101-160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 840-071:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                             TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELERHONE: (212) 840-3333
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 530 Fil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
            LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 42 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGGCGCCAACCTGCTAGGGATTT 24
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Similarity 82.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: GENETICALLY ENGINEERED VACCINE INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCATCAAGCAGCTAGGGATTT 31
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Gettig, Russell Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limbach, Keith J.
Johnson, Gerard P.
Pincus, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Taisne, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perkus, Marion E.
Taylor, Jill
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linear
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iviere, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.6;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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RESULT 7 US-09-758-282B-151

GENERAL INFORMATION: Sequence 151,

APPLICANT: Ma, Wu-Po APPLICANT: Lyamichev

APPLICANT:

Lyamichev, Victor I.
Kaiser, Michael W.
Lyamicheva, Natalie E.
Allawi, Hatim T.

Schaefer, James J. Neri, Bruce P.

PPLICANT

Patent No. 663546

Application US/09758282E

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US-08-455-968E-62/c
                                                                                                                                   US-08-455-968E-62
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,968E

FILING DATE: 30-MAY-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                   Best Local Similarity
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62,
                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harrington, John L.
APPLICANT: Hsieh, Chih-Lin
APPLICANT: Lieber, Michael
TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
NUMBER OF SEQUENCES: 63
                                                                                                                                                 MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                              LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
   3
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                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5874283
CGACCTGCAGCCTGCTAGAGATTTT
                                   CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCGCCAACCTGCTAGGGATTT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two Embarcadero Center, 8th Floor
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                                                                    Conservative
                                                                                                                                                                  linear
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82.6%;
                                                                                   76.0%;
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                                                                  0; Mismatches
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                                                                                   Score 15.4;
Pred. No. 8
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Pred. No. 22;
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                                                                                                 Length 33;
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                                                                    Gaps
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Length 70; Indels

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US-09-393-171-22
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                                                        NUMBER OF SEQ ID NOS: 25
SEQ ID NO 22
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-552-950-22
                                                                                                                                                                                                                                                                Sequence 22, Applicate Patent No. 6673569
GENERAL INFORMATION:
                                                                                                  APPLICANT: KUROKAWA, Yolchi
APPLICANT: YANAGI, Hideki
APPLICANT: YURA, Takashi
TITLE OF INVENTION: DabA/DsbB/DsbC/DsbD expression plasmid
PILE REFERENCE: 1422-391P
CURRENT FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: US/09/393,171
EARLIER APPLICATION NUMBER: JP 10/255702
EARLIER FILING DATE: 1998-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.6%; Score 15.4; Best Local Similarity 76.0%; Pred. No. 88; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: US-09-758-282B-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09552950
Patent No. 6541248
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 674524-2004
               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 61.6%; Score 15.4; Best Local Similarity 94.1%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Enzymes for the Detection of Nucleic Acid Sequences FILE REFERENCE: FORS 04931
CURRENT APPLICATION NUMBER: US/09/758,282B
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 09/577,304
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                    12 CGGGCCCGCCACTGCTAGAGATTTT 36
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                     2, Application US/09393171
_6673569
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S
                                               Query Match
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US-08-068-945A-13/c
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                                                                                                                                                                                                  TELEFAX: (212)354-8113 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-393-171-22
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: SE 9201809-2
PRIOR APPLICATION UNMER: SE 9201809-2
PRIOR APPLICATION DATA:
APPLICATION UNMER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: SE 9202088-2
PRIOR APPLICATION DATA:
APPLICATION UNMER: SE 9202088-2
PRIOR APPLICATION UNMER: SE 9202088-2
PRIOR APPLICATION UNMER: SE 9202088-2
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Matches
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                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPACTABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
     Local Similarity 84.2%;
les 16; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tornell, Jan
TITLE OF INVENTION: New DNA Sequences
NUMBER OF SEQUENCES: 58
                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 AV
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States
ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                          H: 24 base pairs
nucleic acid
DEDNESS: single
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Carlsson, Peter
Enerback, Sven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lidberg, Ulf
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                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                          19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                           SE 9300902-5
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75.0%;
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       0,
Score 14.2; DB 1;
Pred. No. 3.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                    1103326-052
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Pred. No. 3.2e+02;
0; Mismatches 6;
                                Length 24;
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GGCGCCAACCTGCTAGGGA 21 GGCGCCCAGCTGCGAGGGA

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RESULT 11
US-08-442-806-13/c
                                                                                           TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-442-806-13
                                                                                                                                     TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Patent No. 5
                               Matches
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILLING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILLING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILLING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILLING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDBER: US 08/068,945
FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                              Local Similarity
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                     NAME: Sterner, Richard
REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United ZIP: 10036-2787
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STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New Yor
                                                                                                                                                                                                                                      TELEPHONE:
                               16; Conservative
3 GGCGCCAACCTGCTAGGGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bjursell,
Carlsson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
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Tornell, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lidberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enerback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TION:
                                                                                                                                                                                                                                        (212)819-8783
                                                                                                          DNA (genomic)
                                             56.8%;
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Ulf
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Encoding Hum
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Peter
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                                                                                                                                                                                                          13:
                              0; Mismatches
                                              Score 14.2;
Pred. No. 3
                                                                                                                                                                                                                                                                       1103326-052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BSSL/CEL
                                           3.3e+02;
                                                            DB 1;
                                                          Length 24;
                              Indels
                              <u>,</u>
                              Gaps
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                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: 
; OTHER INFORMATION: oligonucleotide 
US-09-625-188-27
                                                                                                                                                                                                                                                                                                                                                                      US-09-625-188-27; Sequence 27, A
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US-08-748-068-14
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-748-068-14
Query Match
Best Local Similarity 7/...
Thes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACENTIA Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,068
FILING DATE: 12-NOV-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMMBER: 08/256,959
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: GB 92 02033.8
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 04702.6
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO.27
LENGTH: 65
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: No. 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                             FILE REFERENCE: PB/5-31285P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                      LENGTH: 65
                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 92
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Ch
NUMBER OF SEQUENCES: 1:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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les 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 base pairs
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                                       56.0%;
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Pred. No. 3.5e+02
0; Mismatches
                       Score 14; DB 4;
Pred. No. 5e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                     Length 65;
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Indels

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Gaps

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CGGGCGCCAACCTGCTAGGGAT 22

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RESULT 15
US-08-479-017-18/c
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            Sequence 18, Application US/08479017
Patent NO. 6143872
GENERAL INFORMATION:
APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HANGSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 55.2%; Score 13.8; DB 1; Length 38; Best Local Similarity 88.2%; Pred. No. 5.7e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/137,175A
FILING DATE: 26-OCT-1993
CLASSIFICATION UNMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: BARBOUR=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-628-5197
TELEFAX: 202-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
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APPLICANT: BERGSTROEM, Sven
APPLICANT: HANSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                               20 CAACCTGCTAGCGAATT
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Search completed: August 31, 2004, 04:43:17 Job time : 40.2857 secs
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                               US-08-479-017-18
                                                                                                                                            Query Match 55.2%; Score 13.8; DB 3; Best Local Similarity 88.2%; Pred. No. 5.7e+02; Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BARBOUR=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TET-FERV. 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROWDY AND STREET: 419 Seventh SI CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,017
FILING DATE:
                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-0-1
TELEPHONE: 202-0-37-3528
                                                                           20 CAACCTGCTAGCGAATT
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419 Seventh Street, N.W., Suite 300
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
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                        US-10-001-407-10
US-10-001-407-8
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US-10-001-407-13
US-10-001-407-13
US-10-001-407-18
US-10-272-665-108
US-10-273-321-108
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Sequence 10, Appl
Sequence 8, Appli
Sequence 9, Appli
Sequence 15, Appl
Sequence 14, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 108, App
Sequence 108, App
Sequence 109, App
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115 116 116 116 117 117 117 117 117 117 117	15 15 15 16 16 16 16 16 16
US-10-351-364-23 US-10-351-196-24 US-10-351-196-24 US-10-279-992A-10 US-10-286-332A-74 US-10-286-332A-74 US-10-286-915-74 US-10-286-915-74 US-09-931-325A-99 US-09-930-915A-140 US-10-806-006-140 US-10-806-006-140 US-10-805-913-140 US-09-931-325A-98	-10-273 -10-273 -09-864 -09-758 -09-864 -10-084 -10-351 -10-126 -10-126
Sequence 24, Appl Sequence 26, Appl Sequence 10, Appl Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl Sequence 140, Appl Sequence 140, Appl Sequence 255, App Sequence 285, App Sequence 285, App Sequence 140, Appl Sequence 140, Appl Sequence 284, Appl	N

# ALIGNMENTS

```
RESULT 1

US-10-001-407-10

; Sequence 10, Application US/10001407
; Sequence 10, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
    APPLICANT: Yang, Yeasing
    APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT PILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-33
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTMARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; SEQ ID NO 10
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: HIV-2
US-10-001-407-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Gaps 0;

1 CGGGCGCCAACCTGCTAGGGATTTT 25

Db 1 CGGGCGCCAACCTGCTAGGGATTTT 25
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RESULT 2 US-10-001-407-8/c ; Sequence 8, Application US/10001407 ; Publication No. US20020177127A1

GENERAL INFORMATION:

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US-10-001-407-15

Sequence 15, Application US/10001407

Publication No. US20020177127A1

GENERAL INFORMATION:

APPLICANT: Yang, Yeasing

APPLICANT: Burrell, Terrie

TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
IIILE OF INVENTION: Compositions and Methods for Detecting
IIILE OF INVENTION: Compositions and Methods for Detecting
IIILE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
IIILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR APPLICATION NUMBER: 60/240,058
PRIOR FILING DATE: 2001-10-3
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
VUMBER OF SEQ ID NOS: 34
SOPTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HENGTH: 34
TYPE: DNA
CORGANISM: HIV-2
US-10-001-407-9
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APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
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; ORGANISM: HIV-2
US-10-001-407-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10001407
Publication No. US20020177127A1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 8 LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                          1 CGGGCGCCAACCTGCTAGGGATTTT 25
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11arity 100.0%; Pred. No. 0.0033;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DE
100.0%; Pred. No. 0.0
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 34; 0.0093;
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Sequence 14, Application US/10001407

Publication No. US20020177127A1

GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie

TITLE OF INVENTION: Compositions and Methods for Detecting
ITITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 25

Type: DNA
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; ORGANISM: HIV-2
US-10-001-407-14
                                                                                                                                                                                                                       Sequence 19, Application US/10001407 Publication No. US20020177127A1 GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
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Best Local Similarity
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SEQ ID NO 15
LENGTH: 52
TYDE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 77 promoter primer having a promoter sequence
OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
OTHER INFORMATION: primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Score 25; D
Best Local Similarity 100.0%; Pred. No. 0.
Matches 25; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%; Score 18; DB 14; Length 25; 100.0%; Pred. No. 34; Live 0; Mismatches 0; Indels
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GENERAL INFORMATION:

APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION UNMBER: 60/242,620
PRIOR APPLICATION UNMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
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LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local S
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LENGTH: 24
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
SOFTMARE: PastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
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PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 CGGGCGCCAACCTGCTAG 58
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                                                                                                                                                                                                                                                                                                                                                                     3 GGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                19;
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82.6%;
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Pred. No.
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Pred. No. 1.8e+02;
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36
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; ORGANISM: Hom sapien
US-10-272-665-108
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US-10-272-665-109
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PRIOR FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILLING DATE: 2000-07-10
PRIOR FILLING DATE: 2000-07-10
PRIOR FILLING DATE: 1999-10-13
PRIOR FILLING DATE: 1999-10-13
PRIOR FILLING DATE: 2000-07-10
PRIOR FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILLING DATE: 2000-09-19
                                                    Publication No. US20030180748A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033E
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 57
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SEQ ID NO 108
LENGTH: 100
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Publication No.
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Best Local Similarity
                                                                                                                                                                         Sequence 109,
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CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES
TITLE OF INVENTION: GENETIC MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/280,058 PRIOR FILING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT FILING DATE: 2002-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: T7 promoter primer having a promoter sequence OTHER INFORMATION: appended at the 5' end of the sequence given as OTHER INFORMATION: SEQ ID NO:13
                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 GGGCGCCACCTGCTAGGGATTTT 57
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                                                                                                                                                                                                                                                                      GGGCGTCAACCTGCAAGGTAT
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                                                                                                                                                   Application US/10272665 o. US20030180748A1
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o. US20030180748A1
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85.7%;
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Pred. No. 1.9e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Score 16.2;
Pred. No. 3.
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PRIOR APPLICATION NUMBER: 09/87,483
PRIOR APPLICATION NUMBER: 09/87,483
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 108
SEQ ID NO 108
LENGTH: 100
TYPE: DNA
ORGANISM. U--
RESULT 12
US-10-273-321-109
(S-10-273-321-109)

Sequence 109, Application US/10273321

Publication No. US20030180749A1

GENERAL INFORMATION:
GENERAL SHORMATION:
APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING
TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033B
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Matches
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-665-109
                                                                                                                                                                                                                                                                                                                                     Query Match
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Publication No. US20
GENERAL INFORMATION:
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-10-273-321-108
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LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING TITLE OF INVENTION: GENETIC MARKERS FILE REFERENCE: 24736-2033B
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CURRENT FILING DATE: 2002-10-15
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PRIOR TILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                   LOCAL
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APPLICATION NUMBER: 60/217,658
FILING DATE: 2000-07-10
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o. US20030180749A1
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ilarity 85.7%;
Conservative
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85.7%;
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Pred. No. 3.1e.
0; Mismatches
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Pred. No. 3.1e+02;
0; Mismatches 3
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3;
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US-10-272-756-109
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; LENGTH: 100
; TYPE: DNA
; ORGANISM: Hom ;
US-10-272-756-108
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US-10-272-756-108
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; ORGANISM: Homo
US-10-273-321-109
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR REPLICATION NUMBER: 60/217,658
PRIOR PRILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 09/63,968
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/63,968
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING |

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT FILING DATE: 2002-10-15

PRIOR PAPPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/217,251

PRIOR APPLICATION NUMBER: 60/217,251

PRIOR APPLICATION NUMBER: 60/217,251

PRIOR APPLICATION NUMBER: 09/663,968

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19
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Best Local Similarity
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64 GGGCGTCAACCTGCAAGGTAT 84
                                       2 GGGCGCCAACCTGCTAGGGAT 22
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o. US20030190644A1
                                                                                       Conservative
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                                                                              64.8%; Score 16.2; DB 15; 85.7%; Pred. No. 3.1e+02; Vative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.8%; Score 16.2; DB 15; 85.7%; Pred. No. 3.1e+02; tive 0; Mismatches 3;
                                                                                                                        Length 100;
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Sequence 109, Application US/10272756 Publication No. US20030190644A1 GENERAL INFORMATION:

APPLICANT: Braun et al

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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-109
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Search completed: August 31, 2004, 06:17:02 Job time: 1823.08 secs
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US-10-273-228-108
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR PELICATION NUMBER: 60/217,658
PRIOR PELICATION NUMBER: 60/217,658
PRIOR PELICATION NUMBER: 60/159,176
PRIOR PELICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR SPLICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 60/217,251
                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 100
; TYPE: DNA
; ORGANISM: Hom sapien
US-10-273-228-108
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PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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Best Local Similarity 85.7
Matches 18; Conservative
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Best Local Similarity
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SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033D
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CURRENT FILING DATE: 2002-10-15
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                                                                                                           GGGCGTCAACCTGCAAGGTAT 84
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85.7%; Pred. No. 3.1e+02;
htive 0; Mismatches 3;
                                                                                                                                                                                                                                         Score 16.2; DB 16;
Pred. No. 3.1e+02;
0; Mismatches 3;
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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Maximum DB seq length: 100
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No.

is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1 AX49427 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	C 444443337654321098765432	Result S
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                                                                                          Bee,G.G., Yang,Y.Y., Kolk,D.P., Giachetti,C. and Detection of hiv-1 by nucleic acid amplification Patent: WO 0104361-A B 18-JAN-2001; Gen-Probe Incorporated (US); Bee, Gary G. (US); Kolk, Dan P. (US); Giachetti, Cristina (US) Sherrol Hoffa (US)
                                                                                                                                                                                     synthetic construct synthetic construct
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Sequence 8 from Patent WO0104361.
AX074095
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Sequence 8
AR400936
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Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.
Detection of HIV-1 by nucleic acid amplification
Patent: US 6623920-A 8 23-SEP-2003;
Location/Qualifiers
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ilarity 100.0%;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic amplification oligomer with 5'
sequence, for HIV-1 LTR region"
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="unknown"
/mol_type="genomic
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a appended at the 5' end of an HIV-2
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/mol_type="genomic
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Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDetection of HIV-1 by nucleic acid amplification Patent: US 6623920-A 26 23-SEP-2003;

Location/Qualifiers
               AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT
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be Incorporated (US)
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/db xref="texon:32630"
/note="T7 promoter primer having a promoter sequence appended at the 5' end of the sequence given as SEQ NO:12"
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/mol_type="unassigned DNA"
                                                         Score 36.4; DB 6;
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Pred. No. 0.0016;
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1 (bases 1 to 54)

Daniel, L.K. and Timothy, J.F.

Probe for detecting oligonucleotide

Patent: JP 1999046778-A 2 23-FEB-199
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Artificial Sequence
JP 199046778-A/2
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11-JUL-1999 US 379501
DANIEL LOUIS KASHIAN,TIMOTHY
C12N15/09,C12Q1/68,C12N15/00
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                                                                                                                       /organism='Artificial Sequence'
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/db xref="taxon:32630"
/noTe="synthetic amplification oligomer with sequence, for HIV-1 LTR region"
                                                                  /organism="synthetic construct"
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Pred. No. 0.0016;
0; Mismatches 1;
Score 36; DB 6; Le
Pred. No. 0.0023;
0; Mismatches 10;
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AX397773
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AR344818
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AR344818
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Sequence
AR352014
                                                                                                                                                                                                                                                  Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G. Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
Patent: US 6582920-A 7, 24-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT 52
synthetic construct
                       AX397773.1
                                                                                                                                                                                                                                                                                                                                  Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: US 6589734-A 2 08-JUL-2003;
Location/Qualifiers
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Kacian,D.L., Fultz,T.J. and McDonough,S.H.
Detection of HIV
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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from Patent WO0220852
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Pred. No. 0.0023;
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PF 28-
PR 28-
PR 28-
PR 28-
CC C1;
CC C1;
CC Cet
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              AR307449
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                                                                                                                                                                                                                                                                                                                                                 artificial sequences.

1 (bases 1 to 49)
Harvey, R.C. and Jr, T.J.C.
Nucleic acid sequence for detecting genetic biological samples
Patent: JP 2002535014-A 38 22-OCT-2002;
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct synthetic construct
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JP 2002535014-A/38.
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Nucleic acid sequence for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biological samples.
                                                                           AATTTAATACGACTCACTATAGGGAGACGGGCGCAACCTG 41
                                                              aaattaatacgactcactatagggagactgreggctgacctg
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Artificial Sequence
JP 2002535014-A/38
22-OCT-2002
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28-JAN-1999 US 60/117640
RICHARD C HARVEY-THOMAS JJ CLARK JR
C12N15/09,C12Q1/68,C12N15/00
Description of Artificial Sequence: synthetic construct
promoter Location/Qualifiers
Location/Qualifiers
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nilarity 76.5%;
Conservative (
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Protease
sequence"
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for cancer in
      PAT 12-JUN-2003
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Query Match
Best Local Similarity
Matches 35; Conserv
A99135
Sequence 9 from Patent WO9907898.
A99135
A99135.1 GI:6782088
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Detection of mycobacterium avium subspecies

Patent: WO 0034517-A 78 15-JUN-2000;

GEZONDHEIDSDIENST VOOR DIEREN (NL), MAANEN CORNELIS VAN (NL), PARIS SOM TJWAN (NL), WAGTER LUCAS HENDRIK ALBERT (NL), MICROSCREEN B V (NL), SCHUT FREDERIK (NL), BRINKHOF JOHANNES MICHIEL ANTH (NL); ENSING HENRIETTE ZWAANTINA (NL); KOOPMANS HENDRIK HIDDO (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclass....
1 (base 1 to 49)
1 (base 1 to 49)
Harvey,R.C. and Clark,T.J. Jr.
Nucleic acid sequences for detecting genetic a biological sample
Patent: US 6551778-A 38 22-APR-2003;
Location/Qualifiers
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AX025599
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AR307449
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ilarity 85.4%;
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/db_xref="taxon:32630"
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/mol_type="genomic
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from Patent WO0034517.
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ACCESSION
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AUTHORS
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AUTHORS
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BD080307
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Search completed: August 31, 2004, 02:04:25 Job time : 1096.38 secs
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Best Local S
Matches 33
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                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                    artificial sequences.

CE 1 (bases 1 to 47)

RS Goudemit, J., Oudshoorn, P., Jurriaans, S. and Lukashov, V.V.

Nucleic acid sequences usable as primers and probes for amplifying and detecting all HIV-1 subtypes

AL Patent: JP 2001512701-A 9 28-AUG-2001;

AKZO NOBEL NV

OS Artificial Sequence
PN JP 2001512701-A/9

PD 28-AUG-2001

PF 05-AUG-1998 JP 2000506380

PF 08-AUG-1997 EP 9720455.8

PI JAAP GOUDSMIT, PIETER OUDSHORN, SUZANNE JURRIAANS, PI

VLADIMIR VLADIMIROVICH LUKASHOV

PC C12Q1/68,C12N15/09,C12N15/00

CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key

FT source //organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unclassified.

1 (bases 1 to 47)

1 (bases 5 to 47)

1 (bases 1 to 47)

JURRIAANS, S. and Goudsmit, J.

NUCLEIC ACID SEQUENCES THAT CAN BE USED AS PRIMERS AND PROBES IN
THE AMPLIFICATION AND DETECTION OF ALL SUBTYPES OF HIV-1

PATENT: WO 9907888-A 9 18-FEB-1999;

JURRIAANS SUZANNE (NL); AKZO NOBEL NV (NL)

Location/Qualifiers
                                                                     N
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47 bp DNA linear PAT 27-AUG-2002 Nucleic acid sequences usable as primers and probes for amplifying and detecting all HIV-1 subtypes.
BD080307
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                                                                                                                                            Conservative
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Location/Qualifiers
                                                                                                                                                                                                                              /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32644"
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91.7%; Pred. No. 0.19;
tive 0; Mismatches 3;
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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1: geneseqn1980s:*
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AAQ86607
AAT15552
AAX23172
AAD62557
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AAA63315
AAX26214
ADE48105
AAQ56491
AAT91790
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AAL45469
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AAF56540
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Aaf56588
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Human imm
Human imm
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HIV regio
HIV-1 pro
HIV-1 pro
HIV-1 pol
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Human imm
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HIV-1
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AAQ86640	ABT12953	AAT91784	ACC43281	AAA89903	AAX57024	AAQ57043	AAQ50478	ABS57299	AAC93118	AAC97508	AAA77716	AAC58539	AAZ23689	AAL45499	ABK53137	AAL45467	ABK53105	AAD62570	AAX23185	AAX23208	2540000
Aaq86640	Abt12953	Aat91784	_	Aaa89903		Aaq57043	Aaq50478	Abs57299	Aac93118	Aac97508	Aaa77716	Aac58539	Aaz23689	Aal45499	Abk53137	Aal45467	Abk53105	Aad62570	Aax23185	Aax23208	Savous
Promoter	Mycobact	Primer BB	Nucleoti	Amplifica	WO9923258	M. tuberc	Promoter-	Primer pl	Human PRO	Human PRC	Human PRC	Human DNA	Human pri	HIV-1 pol	HIV-1 pro	HIV-1 gag	HIV-1 Gag	Human imm	HIV regio	CML t (14	C

## ALIGNMENTS

RESULT 1 ABK93891

ABK93891;

ABK93891

standard;

DNA; 52 ВP

29-AUG-2003 26-AUG-2002

(revised)
(first entry)

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Yang
                                                                                                                                23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
                                                                                                                                                  22-OCT-2001;
                                                                                                                                                               02-MAY-2002.
                                                                                                                                                                           WO200234951-A2
                                                                                                                                                                                      Human immunodeficiency virus 2.
                                                                                                                                                                                                  Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                   Human immunodeficiency virus type 2 detection probe
                                                                                                                     (GENP-) GEN-PROBE INC
                                                                                                        ΥΥ,
                                                                                                        Burrell TA;
                                                                                                                                                   2001WO-US045396
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The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target Claim 11; Page 25; 58pp; English. duplex.

WPI; 2002-489953/52.

and D of HIV-2. The method is useful for amplifying and detecting the NI in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HEV) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)

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Query Match
Best Local S
Matches 49
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Matches 52
                                                                                  The present invention provides probes and PCR primars for use in the detection of HIV-1. These are shown in AAF56533-AAF56589. They can used to diagnose HIV infection and to ensure that blood and blood products do not contain the virus, thus enabling the prevention of infection during blood transfusions. (Updated on 11-SEP-2003 to standardise OS field)
                                                                Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                Detecting HIV-1 nucleic acids in biological samples useful for diagnosing HIV-1 infection involves using nucleic acid capture oligomers, amplification oligomers and probe oligomers.
                                                                                                                                                    Claim 5; Page 50; 60pp; English.
                                                                                                                                                                                                                                  Bee
                                                                                                                                                                                                                                                                                (BEEG/)
                                                                                                                                                                                                                                                                                                                                   07-JUL-2000; 2000WO-US018685.
                                                                                                                                                                                                                                                   (MCDO/)
                                                                                                                                                                                                                                                                                                                   09-JUL-1999;
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18-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                                                                                                                          GEN-PROBE INC.

BEE G G.

YANG Y Y.

KOLK D P.

GIACHETTI C.
                                                                                                                                                                                                                                                                                                                                                                                          immunodeficiency virus
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                                          Similarity
1 AATTTAATACGACTCACTATAGGGAGACGCGCCGACCCTGCTAGGGATTTT
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94.2%;
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                             Score 36.4; DE
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Pred. No. 1.5e-12;
; Mismatches 0;
                          3.6e-06;
1;
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AAF56558; AAF56558

standard;

DNA;

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В₽

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RESULT 3
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AID ABK9
XX ABK9
XX ABK9
XX ABK9
XX ABK9
XX Huma
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RESULT 4
AAF56558
ID AAF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide contacting the amplified NA; or providing a contacting the probe to form probe and detectable label, hybridising HIV-2 NA with the contact of the probe to form probe: target duplex, and detecting the duplex. The method is useful for detecting the probe to a blood contact such as plasma or serum, and also for detecting subtypes A, B, C cand D of HIV-2. The method is useful for amplifying and detecting the NA contact synthesise amplicons corresponding to polymucleotides of currelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C curselated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C curve (HCV). ABK93977-ABK93910 represent HIV-2 detection probes of the vvv
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting human immunodeficiency virus-2 nucleic acids in a sample, amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001; 2001WO-US045396,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2 detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200234951-A2
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26-AUG-2002
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                                                                                                                                                                                                                              1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT
                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                             AATTTAATACGACTCACTATAGGGAGACGGGCGCCA--CTGCTAGAGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 15 A; 10 C;
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                                                                                                                                                                                                                                                                                                                                            70.0%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   12 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                           Pred. No. 8.60
0; Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 36.4;
Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                         8.6e-06;
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RESULT 5
AAV6630
ID AAV6
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XX AAV6
XX Huma
XX Huma
XX Huma
XX Regi
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COS Synt
XX US58
PN US58
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PN US58
XX O6-J-C
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides probes and PCR primers for use in the detection of HIV-1. These are shown in AAP56533-AAP56589. They can be used to diagnose HIV infection and to ensure that blood and blood products do not contain the virus, thus enabling the prevention of HIV infection during blood transfusions. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting HIV-1 nucleic acids in biological samples useful for diagnosing HIV-1 infection involves using nucleic acid capture oligomers, amplification oligomers and probe oligomers.
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                       06-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BEEG/)
(YANG/)
(KOLK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2003
18-APR-2001
  06-JUN-1995;
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus region 1 (+)
                                                                                                                                                                                                                                                                                                                                                                                                         AAV66330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV66330 standard; DNA; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bee GG,
                                                 20-OCT-1998.
                                                                                                                                                     Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; blood screening; PCR primer; probe; ss.
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                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
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BEE G G.
YANG Y Y.
KOLK D P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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MCDONOUGH S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTAATACGACTCACTATAGGGAGACGGGCGCCA--CTGCTAGAGATTTT 50
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                                                                                                                                                                                                                                                   block
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(first entry)
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  9508-00469067
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                                                                                                                                                                                                                                                                                                                                                    entry)
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94.2%;
                                                                                                                                                                                                                                                      template;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒP
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                      autocatalytic RNA amplification;
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                                                                                                                                                                                                                                                                                                  primer.
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RESULT 6
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DT 25-M
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                                                         WPI; 1995-130686/17.
                                                                                                                                                                                                                                    11-JUL-1989;
10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus (HIV) region 1 plus strand primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
15-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methods are used to amplify nucleic acids, especially RNA,
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10-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          US5399491-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer; autocatalytic; target; HIV; 88.
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                                                                                                                                                                                                                                                                                                                      19-MAR-1992;
                                                                                                                                                                             (GENP-) GEN-PROBE INC
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nes 42; Conserv
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                                                                                                             Kacian DL;
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(first entry)
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90US-00550837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; UB -. Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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0

Amplification of nucleic acid targets - using

a reverse transcriptase

FXSXSSSSSSXX

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RESULT 7
AAT15552
ID AAT1
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Best Local S
Matches 42
The present sequence is a primer for the human immunodeficiency virus region 1, which was used to demonstrate an improved method for synthesising multiple copies of a RNA target sequence. The method terminal portion of the target with a primer which hybridises to the 3'-portion of the DNA primer extension prod. reverse transcriptase, RNase H and transcriptase. It can be used as a component of an assay to detect forensic samples. It also has the advantages of being autocatalytic, transcriptase and avoids repetitive manipulations of reaction conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to correct pf field.)
                                                                                                                                                                                                                                                                                                                                                                Auto-catalytic synthesis of multiple copies of an RNA target sequence - uses cooperative action of a DNA and RNA polymerase in presence of RNase H, useful for detection of target sequence e.g. in clinical or
                                                                                                                                                                                                                                                                                                                Example; Col 9-10; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5480784-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus, HIV; region 1; primer; auto-catalytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT15552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ86607-09 are primers and a probe for the human immunodeficiency virus region 1. They are used to produce autocatalytic oligonucleotides which require no change in the experimental conditions i.e.constant temperature, pH and ionic strength. These sequences are useful in generating multiple copies of specific nucleic acid target sequences. (Updated on 25-MAR-2003 to correct pF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT15552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with RNase H activity and a RNA polymerase at constant temp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTAATACGACTCACTATAGGGAGACAAGGGACTTTCCGGCTGGGGACTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kacian DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00379501.
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Pred. No. 1.3e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region 1 (+) primer.
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                                                                                                                                                                                                                                              This invention describes a novel method for the autocatalytic amplification of an RNA target in a transcription-based amplification system without thermalcycling. The method generates oligonuclectides for cloning. Typical applications are the detection of genetic or infectious diseases, the monitoring of responses to therapy, the quantitation or diseases, the incroorganisms in foods, forensic studies and the provide many copies of selected RNA targets under conditions of the invention temperature, ionic strength and ph. Specific amplification of RNA targets increases sensitivity, convenience, accuracy and the reliability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                     Sequence 54 BP; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1989;
10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5888779-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Autocatalytic amplification; transcription-based amplification; thermalcycling; diagnostic; environmental testing; probe; detection; genetic disease; infectious disease; microorganism; food; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV region 1 primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1999
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                                                                                                               42;
                                                                                                                                 Similarity
                              AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autocatalytic amplification of RNA targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTTAATACGACTCACTATAGGGAGACAAGGGACTTTCCGCTGGGGGACTTT
                                                                                                     69.2%;
ilarity 80.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-00379501.
90US-00550837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00461654
                                                                                                                                                                                                A; 12 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 12 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.2%;
                                                                                                                                                                                      13 G; 14 T; 0 U; 0 Other;
                                                                                                     <u>,</u>
                                                                                             Score 36; DB 2; Lo
Pred. No. 1.3e-05;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                      Length 54
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                                                                                             Indels
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52
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                                                                                      Gaps
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RESULT 10
ABK53107
ID ABK53
XX
AC ABK53
XX
AC ABK53
XX
DT 29-AU
DT 12-AU
XX
DE HIV-1
XX
HIV;
KW HIV;
KW rever
XX
XX
CS Human
XX
PD US200
PM US200
PM O9-MA
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                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to oligonucleotides useful in amplifying and detecting human immunodeficiency virus (HIV) nucleic acid in a sample. The invention is used for environmental testing, diagnostic testing, research studies and for the preparation of reagents or materials for cloning or other purposes. The present sequence is HIV region specific
                                                                                                                     HIV-1 protease
                                                                                                                                                                                                                                                                                                                                                                         Sequence 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotide probe, useful in detecting HIV nucleic acid sample and for environmental and diagnostic testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kacian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1989;
10-JUL-1990;
            09-MAY-2002
                                                                                  HIV; human immunodeficiency virus; ss; primer; gag; pol; protease; reverse transcriptase; infection; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                  cloning or other PCR primer. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-810379/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus (HIV) region 1 specific PCR primer #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD62557 standard; DNA;
                                     US2002055095-A1
                                                           Human immunodeficiency virus 1.
                                                                                                                                               29-AUG-2003
12-AUG-2002
                                                                                                                                                                                    ABK53107;
                                                                                                                                                                                                           ABK53107 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENP-) GEN-PROBE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnostic testing; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amplification; human immunodeficiency virus; environmental testing; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                       AATTTAATACGACTCACTATAGGGAGACGGGCCCAACCTGCTAGGGATTTT 52
                                                                                                                                                                                                                                                                        AATTTAATACGACTCACTATAGGGAGACAAGGGACTTTCCGCTGGGGACTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Col 9;
                                                                                                                                                                                                                                                                                                                                                                          BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                               (revised)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00379501.
90US-00550837.
95US-00469067.
                                                                                                                      gene specific oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00168947
                                                                                                                                                                                                                                                                                                                                                                                                 purposes. The pre
sequence is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62pp;
                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                                                                                                                                                                                                                     Score 36; DB 9;
Pred. No. 1.3e-05;
0; Mismatches 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        HIV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang
                                                                                                                                                                                                                                                                                                                                                             probe;
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06-JUN-2002
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                                                                           01-SEP-2000; 2000WO-US024117
                                                                                                                               01-SEP-2000; 2000WO-US024117.
                                                                                                                                                                                                                                WO200220852-A1.
                                                                                                                                                                                                                                                                                    Enterobacteria phage T7.
                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1 pol gene protease amplification oligomer SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL45469;
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1 and probes for detecting
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BABOLA O.
TRAN N.
GEN-PROBE INC
BIOMERIEUX SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTT
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                                                                                                                                                                                                                                                                                                                                                                                     gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     pol gene; PCR; primer; drug resistance; genetic subtype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for amplifying a nucleotide sequence from HIV-
the amplified product are specific for gag and
to detect different subtypes of HIV-1.
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Pred. No. 0
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Best Local &
Matches 39
       primers and primers of
The present invention is concerned with the detection of nucleic acid markers for prostate and breast cancer, and PCR primers and probes which are able to detect and quantify these markers. Prostate specific antigen (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein -2 (hK2) have all been linked to prostate and breast cancers, and the primers and probes of the invention are able to detect the abnormal presence of mRNA expressed by their coding sequences in tissues other
                                                                                                         Detecting prostate-specific antigen (PSA), prostate specific membrane antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using probe molecules, useful for the diagnosis of prostate and breast cancers.
                                                                                               Claim 1; Page 13;
                                                                                                                                                                                                                                   28-JAN-1999,
                                                                                                                                                                                                                                                       28-JAN-2000;
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                                                                                                                                                                                                                                                                                                   WO200044940-A2
                                                                                                                                                                                                                                                                                                                                                       Prostate specific antigen;
glandular kallikrein-2; hK
                                                                                                                                                                                                              (GENP-)
                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of nucleic acid oligomers which can be used to amplify the gag and pol genes of human immunodeficiency virus type I (HIV-1). These are used to detect regions of the gag and pol genes, especially regions associated with drug resistance, and also for identifying genetic subtypes of the virus. The present sequence is an oligomer of the invention. (Updated on 29-AUG-2003 to standardise os
                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                     Clark TJ;
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                                                                                                                                                                                                                                                                                                                                                                                       specific antigen
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                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                         hK2;
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                                                                                                                                                                                                                                                                                                                                                                   PSA;
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                                                                                                                                                                                                                                                                                                                                                  SA; prostate-specific membrane antigen; PSMA;
prostate cancer; breast cancer; probe;
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Pred. No. 0.00
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Matches 35
                                                                                               The present sequence is a PCR primer used in the amplification of the Mycobacterium avium subsp. paratuberculosis 23S rRNA gene. This gene contains several mutations when compared to other Mycobacterium avium subspecies, and some are unique enough to allow the development of a probe which enables specific identification of the presence of paratuberculosis. The organism is responsible for Johne's disease in runinants, especially cows, and is possibly transmitted to humans where it may lead to Crohn's disease. Efficient detection of the bacterium, using a probe designed using this sequence, can be used to identify infected animals so that they can be removed from the herd and destroyed
                                                                                       Sequence 52
                                                                                                                                                                                                                  Example 1; Fig 6; 81pp; English.
                                                                                                                                                                                                                                     Detection of Mycobacterium avium paratuberculosis papecific 23S rRNA mutations at positions 754, 1363 diagnosis of Johne's disease.
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Brinkhof JMA, Van
                                                                                                                                                                                                                                                                                    WPI; 2000-423446/36.
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                                                                                                                                                                                                                                                                                                                                        (GEZO-)
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ÁTTCTAATACGACTCACTATAGGGAGAAGGGCTTCACCCTG
               AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG
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                                           60.4%;
milarity 85.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate. This enables the presence in the detection of metastases
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                                       Score 31.4; DB 3
Pred. No. 0.0013;
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XX Prime
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Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAX26206 to AAX26217 represent claimed oligonucleotides that can be used as primers and probes in the amplification and detection of all subtypes of human immunodeficiency virus type 1 (HIV-1). The oligos are substantially complementary to a sequence of the long terminal repeat (LTR) region of a nucleic acid sequence of a HIV genome. The invention provides a method for detection of HIV-1 nucleic acid using these sequences. Unlike prior art primers and probes, these oligos can detect all known subtypes of HIV-1 with high sensitivity and accuracy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide primers and probes complementary to the LTR region HIV-1 - useful for amplification and detection of HIV-1 infections.
                                                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                         Sequence 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goudsmit J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1; nucleic acid amplification; detection; LTR; human immunodeficiency virus type 1; long terminal
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                                                                                          retroviral
                                                                                                                    Primer #1 of the invention.
                                                                                                                                                                        ADE48105;
                                                                                                                                                                                                 ADE48105 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                  ATTCTAATACGACTCACTATAGGGAGAGGGGGCGCCA
                                                                                          nucleic acid; body fluid; primer;
                                                                                                                                                                                                                                                                                                                                                                           BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                             (first
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                                                                                                                                             entry)
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repeat; ss.
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                                                                                                                                                               The present invention relates to detecting and quantifying a nucleic acid in at least one sample comprising administrating the sample to a solid carrier capable of at least in part absorbing the sample and providing at least a representative part of the carrier to a nucleic acid isolation solution to extract a representative amount of the nucleic acid from the carrier. The method is particularly useful for detecting viral nucleic acid, especially retroviral nucleic acid, in a sample such as a body fluid. The present sequence represents a primer of the invention.
                                                                                                                                     Sequence 47 BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Detecting and quantifying a nucleic acid in a sample, useful for detecting viral RNA, comprises administering the sample to a carrier, exposing the carrier to nucleic acid isolation solution to extract an amount of nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-876928/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-2002; 2002EP-00077697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2003; 2003WO-NL000491
                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 1; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Rooij ER, De Baar MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRIM-) PRIMAGEN HOLDING BV.
                                                                   33;
N
                   1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCA
                                                                                   Similarity
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                                                                 Conservative
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Pred. No. 0.0015;
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Search completed: August 31, time : 345.065 secs 2004, 01:37:13

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111914	CG732356	29	100	ω	2	29
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111911	CG729247	29	100	Ü	۲.	27
111910	CG728814	29	100	ω		26
SWAMCA	AA051807	9	97	ω	۲.	25
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CG728803 1119103C1	CG728803	29	88	43.1	22.4	23
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zehl172		10	96		·	15
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zeh0113.	1353162	9	95	ŗ	w.	12
1119152D	G73290	29	90	5	w.	11
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## ALIGNMEN

LOCUS

AJ282330

AJ282330

AGA3A-P1E1-R Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P1E1, mRNA sequence.

AJ282300

VERSION

KEYWORDS

SOURCE

ORGANISM

Anopheles gambiae
ENT.

Anopheles gambiae
ENT.

REPERENCE

AUTHORS

Dimpoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., and Kafatos, F.C.

TITLE

mosquito innate immune-competent cell lines
generated from immune-competent cell lines
generated from immune-competent cell lines
generated: Dimpoulos G
Fotis C. Kafatos laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.

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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                    PCR PRIMETS

FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTGACCCTCACTAAAGGG 3'.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zeh0940.seq.F Zebrafish Embryonic Heart cDNA linear EST 04-JAN-15 cDNA 5', mRNA sequence. A1353756 A1353756.1 GI:4093909 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AATTTAATACGACTCACTATAGGGAGACGGGCGC 34
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                /organism="Danio rerio"
/mol_type="mrNA"
/mb_xref="taxon:7955"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XLI-Blue mrF'"
/clone_ilb="Zebrafish Embryonic Heart cDNA Library"
/clone_ilb="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoR1; Site_2: XhoI, mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). CDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clome_lib="Anopheles gambiae immune competent 4A3A"
/note="Wector: pTTT3D-Bac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
forward priming site which reads from the 3' end of the
CDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
cligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
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/clone="4A3A-P1E1"
/cell line="immune competent 4A3A"
/lab_host="E. coli DH10B"
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directional cloning into pre-digested lambda ZAP
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CG728851
CG728851.1 GI:37
GSS.
Zea mays
                                                                                           Similarity
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: transposon-tagged.
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Tel: 650 723 2227
Fax: 650 725 8221
ATTGTAATACGACTCACTATAGGGCGATTTGCGGCAGCACGGCGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse complemented post-ligation sequence from source sequence. Plate: 1119104 row: 12
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                               AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
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                                                                         Conservative
                                                                                                                                          /Clone lib="119 - RescueMu Grid AA"
/Clone lib="119 - RescueMu Grid AA"
/note="organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
DamHI and BgIII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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Fax: 410 706 1622
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Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
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cDNA 5', mRNA sequence.
CA406952
CA406952.1 GI:24771823
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1119146G02.1EL_x1 1119 -
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Seq primer: GTTGGTACCCGGGAATTC.
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                                                                                                              Contact: Walbot V
Department of Biological Sciences
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Email: walbot@stanford.edu
Very probable ligation site of ends
Reverse complemented post-ligation
                                                                                               Stanford University
                                                                                                                                              Maize genomic sequences
Unpublished (2001)
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                                                  650 723 2227
650 725 8221
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplEx"
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855 California Ave, 1
Tel: 650 723 2227
Fax: 650 725 8221
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CG729102
CG729102.1 GI:37
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Zea mays
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Class:
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                                                                                                                                                                                 Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Walbot
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Unpublished (2001)
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                      Reverse complemented post-ligation Plate: 1119107 row: 3
                                                                                                                                                                                                                                                           Email: walbot@stanford.edu
Very probable ligation site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="119 - RescueMu Grid AA"
/clone lib="119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transposon-tagged.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - |
                                                                                /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/KS5"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /culfivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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                                                             tissue_type="leaf"
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lab_host="DH10B"
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                        found using engineered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RescueMu
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        RescueMu Grid AA"
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                                                                                                                                                                                                                                                             ends cut by single endonuclease
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a; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                            transposon
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REFERENCE
AUTHORS
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Best Local S
Matches 33
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ORGANISM
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A1616894/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                POR PRIMERS

FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Sed primer: 5' GAAATTAACCCTCACTAAAGGG 3'

                            h 47.3%;
Similarity 70.2%;
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Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 96)

Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 bp zehn0783.seq.F Zebrafish Embryonic cDNA 5', mRNA sequence.
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AI616894.1 GI:4626061
EST.
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           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cliew@rics.bwh.harvard.edu
                                                                                                                /dev_stage="embryonic day 3 post-fertilization"
/lab_host="E_coli XLI-Blue mrF/"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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      Pred. No. 47;
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Pred. No. 28;
0; Mismatches
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Heart cDNA Library Danio rerio
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CA336070/c
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TITLE
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VERSION
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AI087772/c
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                                                                                                                                                                                              67
CA336670 79 bp mRNA linear EST 04-NOV-2002 NISC_lu07h08.y1 COGENE 4AR (4EAR) Homo sapiens cDNA clone IMAGE:5607422 5', mRNA sequence. CA336070 CA336070 GI:24554168 EST.
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AI087772
AI087772.1 GI:3426748
BST.
Onchocerca volvulus
Onchocerca volvulus
Conchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Conchocercidae; Onchocerca.
1 (bases 1 to 75)
1 (bases 1 to 75)
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 413583866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lizotte-Waniewski,M. and Williams,S.A.
Genes expressed in adult male stage of Onchocerca volvulus
Unpublished (1998)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
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SWOVAMCAQ02F02SK Onchocerca volvulus adult male cDNA
(SAW98NLW-OVAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02F02 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 4135853786
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                                                                                                                                                                                        AATGTAATACGACTCACTATAGGGCGA 41
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                                                                                                                                                                                                                                                                   45.8%;
ilarity 92.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                  /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10E5 independent recombinants and the average insert size is ~1100bg. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="XLI-Blue MRF/"
/clone lib="Onchocerca volvulus adult male cDNA
(SAM98MLM-OvAM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Onchocerca v./mol_type="mRNA"
/db_xref="taxon:6282"
/db_xref="SWOVAMCAQ02F02"
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                                                                                                                                                                                                                                                                                      Score 23.8;
Pred. No. 87;
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RESULT 10
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AUTHORS
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                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTTAATACGACTCACTATAGGGAGACG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAM12408 row: P column:
Seg primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                       Stanford University
855 California Ave, Palo
                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                            CG733887.1
                                                                                                                                                                                                                                                                                                                                                                                  1119160E10.1EL_x1 1119 -
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Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               Department of Biological Sciences
                                                                                                                   Contact: Walbot V
                                                                                                                                                                           Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                  survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        CG733887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                      Zea mays
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                                                                                                                                                                                           (bases 1 to 86)
650 723 2227
650 725 8221
l: walbot@stanford.edu
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/dev_stage="embryo, 4 weeks postconception"
/lab_host="bH10B"
/clone_lib="COGENE 4AR (4EAR)"
/clone_lib="COGENE 4AR (4EAR)"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.3-1.6 kb.
Normalized to Cotlo. Primary library, non-amplified.
Library constructed by M. Lovett. For moore information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 89;
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TITLE
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                                                                                                                                                             Stanford University
855 California Ave, Palo Alto, CA 9430
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cu
Reverse complemented post-ligation sec
Plate: 1119152 row: 14
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                                                                                                                                            Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                              Department
                                                                                                                                                                                                                                                                                                                                                 Contact: Walbot
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
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ilarity 76.3%;
Conservative
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/clone_lib="1119 - RescueMu Grid AA"
/note="Organ; leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
/mol_type="genomic DNA"
/culfivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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/lab_host="DH10B"
                                                                                organism="Zea mays"
                                                                                                                    ocation/Qualifiers
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0; Mismatches 9
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aceae; PACCAD
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AI353162/c
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BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ton, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAAC 38
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Danio rerio
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                                                            /organism="Danio rerio"

/mol type="mrNA"

/db_xref="taxon:7955"

/db_xref="taxon:7955"

/dev_stage="embryonic day 3 post-fertilization"

/lab_host="E.coli XL1-Blue mrF'"

/lab_host="E.coli XL1-Blue mrF'"

/clone_lib="Zebrafish Embryonic Heart cDNA Library"

/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic

zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP

Express vector. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : cliew@rics.bwh.harvard.edu
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web 'RescueMu,' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double djegsted using BamHI and BglII, and ligated to form circular plasmids. plates with ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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    Score 23.6;
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Pred. No. 1.1e+02;
0; Mismatches 9; Indels
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    B
9;
Length 95;
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Y Danio rerio
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AUTHORS

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                                               AI617314
zehn1391.seq.F Zebrafish
cDNA 5', mRNA sequence.
AI617314
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   Danio rerio
                               AI617314.1
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FORMARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTCTAATACGACTCACTATAGGGCG
Seg primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
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Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
Fax: 6179750995
                                                                                                                                                                                                                                                               Similarity
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Contact: Liew CC
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zeh0701.seq.F Zebrafish
cDNA 5', mRNA sequence.
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synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloming into pre-digested lambda ZAP
Express vector. "
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Pred. No. 1.1e+02;
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CDNA Library Danio rerio
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Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
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                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 96)
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zehl1725 Zebrafish Embryonic Heart
5', mRNA sequence.
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1 (Dases 1 to 96)

1 (Dases 1 to 96)

1 (Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and
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Harvard Medical School
75 Francis St. Boston, MA 02:
Tel: 6177328915
                                                                                                                          Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
Contact: Liew CC
                                                                                                                                                                                                                    Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Liew,C.C.
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FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
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cliew@rics.bwh.harvard.edu
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EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dradaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
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0; Mismatches 14;
                                                               MA 02115,
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Ostariophysi;
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Express vector. "
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; Sequence 26, Application
; Patent No. 6623920
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GENERAL INFORMATION:
APPLICANT: BEE, GATY G.
APPLICANT: YANG, Yeasing Y.
APPLICANT: KOLK, Dan
APPLICANT: KOLK, Dan
APPLICANT: MCDONOUGH, Sherrol H.
APPLICANT: MCDONOUGH, Sherrol H.
TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
CURRENT APPLICATION NUMBER: US/09/611,627
                                                                                                                                                                              AATTTAATACGACTCACTATAGGGAGACGGGCGCCA--CTGCTAGAGATTTT
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Result No.

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US/09611627

라 ઇ	Query Matches	FEATUR OTHER OTHER OTHER OFFER	; SEQ ID NO 8 ; LENGTH: 5 ; TYPE: DNA ; ORGANISM:	,	; CURRENT ; CURRENT	FILE	; APPLICANT:	APPLICANT:	GENERAL INF	RESULT 1 US-09-611-6 ; Sequence		45	c 43	42		39	3 37 8 7	36	ω 4.1	υ u	3 L	30	29	<b>ာ</b>	
1 AATTTAATAC	Match .ocal Similarity .s 49; Conservat	FORMATION: FORMATION: FORMATION: 7-8	: 50 DNA SM: Artificial	ING DATE: SEQ ID NOS PatentIn	CURRENT APPLICATION NUMBER: 05/0 CURRENT FILING DATE: 2000-07-07 PRIOR APPLICATION NUMBER: 60/14	RENCE:		KOLK,	HZ:	1-627-8 ce 8, Application US/0961162 No 6633030		8 53.	53.	28 53.8	8 53.	8 53.	8 53.	8 53.	8 53.	8 53.	50.5	8 53.	8 53.	л	
GACTCACTA	70.0%; 94.2%; ative	escriptic mplificat or HIV-1	Sequence	N 0	0 7	GP103-02.UT	, Cristina [, Sherrol ]		N: Sary G.	n US/0961			ب.	49 1	٠,	.4.	4 م		٠,	<u>.</u>					
AATTTAATACGACTCACTATAGGGAGACGGCGCCAACCTGCTAGGGATTTT	Score 36.4; DB 4; Pred. No. 1.1e-06; 0; Mismatches 1;	Description of Artificial Sequence amplification oligomer with 5' profor HIV-1 LTR region			: US/09/611,62/ -07-07 -0143,072	(00/011 C)	H. H. by			11627	ALIGNMENTS	US-08-683-122-2	US-08-384-541-8	US-08-384-541-7	US-08-384-541-5	US-09-975-408-7	US-08-162-836-6 US-09-710-200-7	US-08-683-124-3	US-08-683-122-3	US-08-692-610-3	US-08-360-051A-23	944-036-3	-08-48	175-08-482-428-14	
GCTAGGGATTTT 52	Length 50; Indels 2; Gaps 1;	nce: synthetic promoter sequence,					ACTO ANDLIETCATION					Sequence 2, Appli Sequence 2, Appli	, œ		'n	.7:	7.0	sequence 3, Appli	. ω	w	16	, ω ,	14	9 1 4	

CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57

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RESULT 4
US-09-944-036-7
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COURRENT FILING DATE: 1998-10-08
FARLIER APPLICATION NUMBER: 08/469,067
FARLIER FILING DATE: 1995-06-06
FARLIER FILING DATE: 1995-07/550,837
FARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
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APPLICANT: BRENTANO, Steven T.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
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Best Local Similarity
Matches 42; Conserv
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Patent No. 6589734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KACIAN, DANIEL L.
APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
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SEQ ID NO 26
ELENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Pred. No. 1.6e-06;
0; Mismatches 10
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Pred. No. 1.1e-06;
0; Mismatches 1;
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US-09-493-491A-38
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US-09-493-491-35
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APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thomas, J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-02_UT
CURRENT APPLICATION NUMBER: US/09/493,491A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/117,640 US
                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09493491A
Patent No. 6551778
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
SOFTMARE: PATENTIN VET. 2.1
SEQ ID NO 7
SEQ ID NO
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CURRENT FILING DATE: 2000-01-28
EARLIER APPLICATION NUMBER: 60/117,640 US
EARLIER FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
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APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thomas, J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-02.UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 639155
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Best Local Similarity
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ORGANISM: Artificial Sequence
FEATURE:
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85.4%; Pred. No. 0.00016;
tive 0; Mismatches 6
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Pred. No. 0.00011;
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APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/09/168,947
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 08/469,067
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 52
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Best Local S
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APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02_UT
CURRENT APPLICATION NUMBER: US/09/944,036
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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TYPE: DNA
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Similarity 85.0%;
34; Conservative
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Pred. No. 0.00016;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.4; DB 4; Length Pred. No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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RESULT 10
US-09-040-220D-7
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Sequence 7, Application US/09040220D
Patent No. 6391311
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VERNET, GUY

TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIO

TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIO

FILE REFERENCE: GP114-02.UT

CURRENT APPLICATION NUMBER: US/09/944,036

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: US 60/229,790

PRIOR RILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 50
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Protease target OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Gag target sequence NAME/KEY: promoter LOCATION: (1)..(29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: promoter LOCATION: (1)..(33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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74.5%;
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Pred. No. 0.00052;
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Pred. No. 0
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CURRENT APPLICATION NUMBER: US/09/265,686
CURRENT PILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
INUMBER: OF SEQ ID NOS: 8
                                                                                                                                                  RESULT 12
US-09-723-749-7
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US-09-265-686-7
                 Sequence 7, Application US/09723749
Patent No. 6620784
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND EMPIFILE REFERENCE: P1122P2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized
Patent_NO. 6455283
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
CURRENT APPLICATION NUMBER: US/09/723,749
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized Patent No. 6391311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ferrara, Napoleone APPLICANT: Kuo, Sophia S. TITLE OF INVENTION: POLYPEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                            Conservative
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ilarity 82.9%;
Conservative
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82.9%;
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                                                                                                                                                                                                                                                                                      Score 29.8; DB 4;
Pred. No. 0.00076;
0; Mismatches 7
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                                                                                                                                                                                                                                                                                                                       DB 4; Length 48;
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CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
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US-08-162-836-10
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                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized
Patent No. 6620784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,836
                                                                                                                                                 TELEPHONE: (213) 489-1600
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Daniel L. Kacian
APPLICANT: Diane L. McAllister
APPLICANT: Sherrol H. McDonough
APPLICANT: Nani Bhushan Dattagupta
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
TITLE OF INVENTION: METHOD, COMPOSITION AND KIT
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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              TYPE: nucleic acid
STRANDEDNESS: single
                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AATTTAATACGACTCACTATAGGGAGACGGGGGGCGCCAACCTG 41
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5554516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3E: Lyon & Lyon
611 West Sixth Street
                                                                                                                                 (213) 955-0440
linear
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                                                                                                                                                                                                       32,327
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Pred. No. 0.00076;
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RESULT 15
US-08-479-105A-6
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                                                                                                                                                                                                                                              US-08-345-861-6
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Sequence 6, Application US/08479105A Patent No. 5908744
GENERAL INFORMATION:
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Best Local Similarity
Matches 35; Conserv
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFFINATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 197/136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA: 07/9:
APPLICATION UNMBER: 07/9:
FILING DATE: August 4, 1:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Philip Hammond
APPLICANT: Thomas B. Ryder
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 611 West S
CITY: Los Angeles
STATE: California
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTA 44
                                                                                                                AATTTAATACGACTCACTATAGGGAGACCAGGCCACTTCCGCTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTAATACGACTCACTATAGGGAGACCAGGCCACTTCCGCTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08345861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Lyon & Lyon
611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                          (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nanibhushan Dattagupta
Diane L. McAllister
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherrol H. McDonough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           56.9%;
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                                                                                                                                                                                                                                                                                                                                             6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29.6; DB 1; Length 47; Pred. No. 0.00092;
                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                            Score 29.6; DB 1;
Pred. No. 0.00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                            Length 47;
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Search completed: August 31, 2004, 04:43:18 Job time: 82.7143 secs

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Gaps

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US-08-479-105A-6
                                                                 Matches
                                                                               Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/925,405
FILING DATE: August 4,1992
APPLICATION NUMBER: 07/855,732
FILING DATE: March 19, 1992
APPLICATION NUMBER: 07/550,837
FILING DATE: July 10, 1990
APPLICATION NUMBER: 07/379,501
FILING DATE: July 11, 1989
ATTORNSY/AGENT INFORMATION:
NAME: Heber, Sheldon 0.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/479,105;
PILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/345,861
FILING DATE: No. 5908744ember 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Did
MEDIUM TYPE: storage
COMPUTER: IBM PC Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID
                                                                               Local Similarity
                                                                                                                                                               LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                     (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diane L. McAllister
Philip Hammond
                                                                 Conservative
                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5" Diskette, 1.44 Mb
                                                                               56.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/479,105A
                                                                                                                                                                                                                                      6.
                                                                 <u>.</u>
                                                                Score 29.6; DB 2;
Pred. No. 0.00092;
n: Mismatches 9;
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                                                                                               Length 47;
                                                                 Indels
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CHASO MINDIE BUNG USFILL

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                    Query
Match
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70.0
70.0
70.0
69.2
61.2
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60.4
58.5
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52
1 aatttaatacgactcactat.....gccaacctgctagggatttt 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               August 31, 2004, 01:37:23; Search time 3789.92 Seconds (without alignments) 67.525 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 . (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        BB
4 US-10-001-407-15
3 US-10-632-658-8
14 US-10-632-658-8
14 US-10-632-658-26
15 US-10-244-490-2
9 US-09-944-036-7
15 US-10-273-707-38
15 US-10-273-707-38
15 US-09-944-036-5
9 US-09-944-036-5
9 US-09-944-036-5
9 US-09-944-036-5
9 US-09-944-036-5
9 US-09-944-036-37
16 US-10-425-975-37
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  Sequence 15, Appli
Sequence 10, Appli
Sequence 8, Appli
Sequence 17, Appli
Sequence 26, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 37, Appli
Sequence 37, Appli
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유 성		us:																							
0 \	Query Ma Best Loc Matches	1	LENGTH: !  TYPE: DNI ORGANISM	NUMBER OF	RIOR	CURREN	FILE	APPLIC APPLIC TITLE	ESULT 1 S-10-001-4 Sequence Publicati		444	44.	40 41	38 39	36 37	ωω 54	3 2 3 3 2 1	30	28	265	23	21 22	19 20	17 18	15 16
1 1 2—2	Match ocal Simi	PEATURE: FEATURE INFORMOTHER I	Q ID NO 15 LENGTH: 52 TYPE: DNA	RE: Fast	APPLIC	APPLIC	REFEREN	CANT: Y	L-407-15 De 15, Apation No.		228	22.6	V 2 B 8	28.2 28	28.2 28.2	28.2 28.2	28.4	28.4	28.4	28.8	28.8	29.2 29	29.4	29.6 29.4	29.8 29.6
ATTTAAT	larit Conse	ATION: ATION: ATION:	T.	SESEO FO	DATE:	ATION N	E: GP1	APPLICANT: Yang, Yeasing APPLICANT: Burrell, Terrie TITLE OF INVENTION: Compositi	.5 Applicat: 10. US200:		53.8	55.8	53.8	54.2 53.8	54.2 54.2	54.2 54.2	54.6	5 4 4 5 6 6	54.6	555	55.4	56.2 55.8	56.5 56.2	56.9	57.3 56.9
ACGACTO	100 y 100 rvative	T7 ] app	Semienc	S: 34 Dr Windows	E: 2000-10 N NUMBER: (	MBER:	Human 17-03.U	asing Terric	ation US/100014 0020177127A1		448	. A. C	3 3 5	56 32	53	48 51	57 61	2 L L	v 	50	48	55	47 45	45 45	48 52
ACTA	0.00	80.00	B D D	B AO	-30 -30	-10-	; I	e	/100 27A1		14 15	۲ <u>.</u> ۲	9 16	9 15	15 15	14 15	14	, L L	15	16	13	15 13	13	13 13	15 15
AATTTAATACGACTCACTATAGGGAGACGGGGCCCAACCTGCTAGGGATTTT	Score 52; DB 14; L Pred. No. 5.5e-13; 0; Mismatches 0;	equence		Version 3.0	280,058	201-10-22 R: 60/242,620	leficiency Virus 2	Methods for De	001407 L	ALIGNMENTS	.4 US-10-075-579-7 S US-10-244-490-5	US-10-461-790-47	US-10-425-975-3	US-10-231-843-7 US-09-944-036-3	US-10-231-843-3 US-10-231-843-25	US-10-006-009-42 US-10-244-490-25	US-10-001-407-18 US-10-077-383-18	US-10-461-/90-49 US-10-363-852-2 US-10-231-843-5	US-10-461-790-38 US-10-077-383-25	US-09-944-036-8 US-10-425-975-8	US-10-632-658-24 US-10-632-658-28	US-10-245-988-2 US-10-461-790-116	US-10-461-790-39 US-10-244-490-39	US-10-461-790-36 US-10-461-790-48	US-10-178-442-7 US-10-231-843-9
TAGGGATTTT 52          TAGGGATTTT 52	Length 52; Indels 0; Gaps 0;	ter sequence 2 complementary					HIV-2)	tecting			Sequence 7, Appli Sequence 5, Appli	6	Sequence 3, Appli	Sequence 7, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 25, Appl	Sequence 42, Appl Sequence 25, Appl	Sequence 18, Appl Sequence 18, Appl	Sequence 2, Appli Sequence 2, Appli	Sequence 25, Appl	Sequence 8, Appli Sequence 8, Appli	Sequence 24, Appl Sequence 28, Appl	Sequence 2, Appli Sequence 116, App	Sequence 39, Appl Sequence 39, Appl	Sequence 36, Appl Sequence 48, Appl	equence equence

US-10-461-790-100

Publication No.

Application US/10461790 DS- US20040029111A1

INFORMATION:

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FEATURE: FEATURE: Peacription of Artificial Sequence: Synthetic OTHER INFORMATION: amplification oligomer with 5' promoter sequence: OTHER INFORMATION: for HIV-1 LTR region
US-10-632-658-8
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/632,658
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/611,627
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: HIV-specific promoter-primer US-10-461-790-100
                                                      Query Match
Best Local Similarity
Conserv
                                                                                                                                                                                                                                                                                            SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/389,393
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 100
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10632658 Publication No. US20040053223A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEE, Gary G.
APPLICANT: YANG, Yeasing Y.
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, Cristina
APPLICANT: MCDONOUGH, Sherrol H.
TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                       LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ho-sing-Loy, Marcy
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Hepatitis B Virus
FILE REFERENCE: GP134-02.UT
CURRENT APPLICATION NUMBER: US/10/461,790
CURRENT FILING DATE: 2003-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Linnen, Jeffer APPLICANT: Kolk, Daniel APPLICANT: Dockter, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                    49;
1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTTAATACGACTCACTATAGGGAGACGGGCGCCA--CTGCTAGAGATTTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dockter, Janel M. Getman, Damon K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshimura, Tadashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jeffery M.
                                                                70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 36.4; DB 13; 94.2%; Pred. No. 4.7e-06;
                                         0,
                                                          Score 36.4; DB 13;
Pred. No. 4.7e-06;
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                                              Mismatches
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                                                                             Length
                                         Indels
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APPLICANT: KOLK, Dan
APPLICANT: KOLK, Dan
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, Cristine
APPLICANT: MCDONOUGH, Sherrol H.
ITILB OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/632,658
CURRENT FILING DATE: 2003-08-01
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Yang, Yeasing

APPLICANT: Burrell, Terrie

ITILE OF INVENTION: Compositions and Methods for Detecting

ITILE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2001-03-30

NUMBER: OF SEQ ID NOS: 34

SOPTWARE: FastSEQ for Windows Version 3.0
                                                                         US-10-632-658-26
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US-10-001-407-17
J Sequence 17, Application US/10001407
Publication No. US20020177127A1
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BEE, Gary G.
APPLICANT: YANG, Yeasin,
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, C
APPLICANT: MCDONOUGH, S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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Best Local Similarity
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                                                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: amplification oligomer with 5' promother information: for HIV-1 LTR region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: T7 promoter primer having a promoter sequence
OTHER INFORMATION: appended at the 5' end of the sequence given as
OTHER INFORMATION: SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AATTTAATACGACTCACTATAGGGAGACGGCGCCAACCTGCTAGGGATTTT 52
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       70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.0%; Score 36.4; DB 14; Length 94.2%; Pred. No. 4.7e-06; tive 0; Mismatches 1; Indels
Score 36.4; DB 13; Pred. No. 4.7e-06;
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Length 51;

Matches

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Conservative

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US-10-244-490-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10244490 Publication No. US20030152916A1 GENERAL INFORMATION:
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                                                                                                                                                                                                             APPLICANT: VERNET, GUY
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR APPLICATION NUMBER: US 60/229,790
RIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/469,067
PRIOR TILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/550,837
PRIOR FILING DATE: 1990-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/09/168,947
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YANG,
APPLICANT: BRENT
APPLICANT: BABOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Protease target
OTHER INFORMATION: Sequence
NAME/KEY: promoter
LOCATION: (1)..(32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 54
TYPE: DNA
                                                                                                        LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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BABOLA, Odile
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O; Mismatches
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7.2e-06;
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RESULT 9
US-10-273-707-38
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LENGTH: 52
                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/10273707 Publication No. US20030104448A1
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Best Local Similarity
                                                        APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thomas, J.
APPLICANT: NUVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-03.DV1
CURRENT APPLICATION NUMBER: US/10/273,707
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 09/493,491
PRIOR APPLICATION NUMBER: 09/493,491
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-28
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TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
RRIOR APPLICATION NUMBER: US/9/944,036
PRIOR PELING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. :
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/229,790 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YANG, Yeasing Y. APPLICANT: BRENTANO, Steve APPLICANT: BABOLA, Odile
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonuclectide primer for Protease target
OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: promoter LOCATION: (1)..(32)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAN, Nathalie
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76.5%;
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Pred. No. 0.00053;
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CCURRENT APPLICATION NUMBER: US/10/244,490

CCURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US/09/168,947

PRIOR APPLICATION NUMBER: US/09/168,947

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 08/469,067

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 07/550,837

PRIOR FILING DATE: 1990-07-10

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 3.0
               Sequence 5, Application US/09944036
Patent NO. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: TRAM, Nathalie
APPLICANT: TRAM, Nathalie
APPLICANT: TRAM, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
CURRENT FILING DATE: 2001-08-31
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; LOCATION: (1)..(28)
US-10-273-707-38
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PRIOR APPLICATION NUMBER: US 60/229,790
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LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/10244490 Publication No. US20030152916A1 GENERAL INFORMATION:
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Best Local Similarity 85.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KACIAN, DANIEL L. APPLICANT: FULTZ, TIMOTHY J APPLICANT: MCDONOUGH, SHERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthesized nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                           1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCCAACCT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.5%;
ilarity 85.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30.4; DB 15; Length Pred. No. 0.0022; Indels 6; Indels
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APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, GUY
ITILE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
ITILE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
NUMBER OF SEQ ID NOS: 70
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
CURRENT: 50
TYPE: DNA
CURRENT SECONDAINE SEQUENCE
US-09-944-036-37
US-09-944-036-37
; Sequence 37, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
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APPLICANT: YANG, Yeasing Y.
APPLICANT: BENTANO, Steven
APPLICANT: BABOLA, Oddie
APPLICANT: TRAN, Nathalie
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US-10-425-975-5
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Best Local S
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Publication No. US20030228574A1
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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32; Conserv
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                                                                                                                                                                                                               58.1%;
91.4%;
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Pred. No. 0.0027;
0; Mismatches 3;
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Pred. No. 0.0027;
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APPLICANT: YANG, Yeasing Y. APPLICANT: BRENTANO, Steve APPLICANT: BABOLA, Odile

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PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
ORDERS OF SEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Protease target
OTHER INFORMATION: sequence
NAME/KEY: promoter
LOCATION: (1)..(33)
US-09-944-036-37
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Best Local S
Matches 38
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
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Best Local S
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TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
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CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/944,036 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-04-28
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APPLICANT: BREN
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                                                                                                                                                       FEATURE: promoter LOCATION: (1)..(33)
                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Protease target OTHER INFORMATION: sequence
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                                                                       Conservative
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74.5%;
                                                                                      58.1%;
                                                                   Score 30.2; DB 16;
Pred. No. 0.0027;
0; Mismatches 13;
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                                                                                                      Length
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 52
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; OTHER INFORMATION: Sequence is synthesized US-10-178-442-7
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CURRENT APPLICATION NUMBER: US/10/178,442
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10178442 Publication No. US20030113870A1 GENERAL INFORMATION:
                                                                            Matches
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND
                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  TYPE: DNA
                                                                          34;
                          1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG
ATTCTAATACGACTCACTATAGGGCGGCGGAATCCAACCTG
                                                                          Conservative
                                                                                            57.3%;
                                                                          .
                                                                                          Score 29.8;
Pred. No. 0.
                                                                        Mismatches
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                                                                                                                DB 15;
                                                                            7; Indels
                                                                                                                Length
  43
                                      41
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                                                                            Gaps
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Search completed: August 31, 2004, 06:17:10 Job time: 3797.92 secs

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